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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodatta/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodatta/2/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodatta/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodatta/2/pubpaa/US06_NEW_PUB.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                 / Cgn2_6/ptodata/2/pubpaa/US09_BUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB_DEP:*
/ Cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB_DEP:*
/ Cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB_DEP:*
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/cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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1144.220 Million cell updates/sec
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1032 1032 1032 1032 1032 1032 1032 1032	Score
100.0	Query Match
2 2 2 2 2 2 2 2 2 2 3 2 3 3 2 3 3 3 3 3	% Query Match Length DB
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US-10-668-778-2 US-09-919-901-7 US-09-919-901-14 US-09-919-901-21 US-09-837-306-354 US-10-191-966-7 US-10-191-966-7 US-10-191-966-21	ID
Sequence 2, Appli Sequence 7, Appli Sequence 14, Appl Sequence 21, Appl Sequence 354, Appl Sequence 7, Appli Sequence 14, Appl Sequence 21, Appl Sequence 523, Appl Sequence 523, Appl Sequence 73, Appl Sequence 2, Appli	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
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US-09-925-298-760	US-10-062-188-2	US-10-491-653-146	US-10-393-449-3	US-10-177-725-3	US-10-656-029-8	US-10-280-482-8	US-09-772-114-9	US-10-877-952-154	US-10-656-029-6	US-10-622-088-114	US-10-280-482-6	US-09-772-114-8	US-10-890-675-2	٠	-10-877-952-	-10-877	US-10-877-952-26	US-10-656-029-4	US-10-280-482-4	US-10-016-668-5	US-09-772-114-7	- 1	US-10-280-482-2	US-09-772-114-6	US-10-477-044-1	US-10-251-385-292	US-10-842-534-9	-10-231-013-	-10-191-966-	US-10-191-966-9	US-10-191-966-2	901-	US-09-919-901-9
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RESULT 1 US-10-668-778-2

; Sequence 2, Application US/10668778 ; Publication No. US20040038317A1 ; GENERAL INFORMATION:

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APPLICANT: Balint, Robert F.
APPLICANT: Her, Jeng-Horng
APPLICANT: Her, Jeng-Horng
APPLICANT: Kalbālos, Inc.
TITLE OF INVENTION: Interaction-Activated Proteins
FILE REFERENCE: 021167-000700US
CURRENT APPLICATION NUMBER: US/10/668,778
CURRENT APPLICATION NUMBER: US/09/526,106
PRIOR FILING DATE: 2000-03-15
PRIOR FILING DATE: 1999-03-15
PRIOR APPLICATION NUMBER: US 60/135,926
PRIOR APPLICATION NUMBER: US 60/135,926
PRIOR APPLICATION NUMBER: US 60/135,926
PRIOR APPLICATION NUMBER: US 60/175,968
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1990-05-13
INUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 263
TYPE: PRT
ORGANISM: Escherichia coli
PRATURE:
OTHER INFORMATION: TEM-1 beta-lactamase
US-10-668-778-2
Query Match
Best Local Similarity 100.0%; Score 1032; DB 15; Length 263;
Best Local Similarity 100.0%; Pred. No. 1.3e-99;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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US-09-919-901-14
Sequence 14, Application US/09919901
Publication No. US20030082518A1
GENERAL INFORMATION:
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US-09-919-901-7
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US-09-919-901-7
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Publication No. US20030082518A1
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Best Local 9
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    APPLICANT: Potts, Karen E. APPLICANT: Jackson, Rober APPLICANT: Patick, Amy K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 286
TYPE: PRT
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Jackson, Rober
Patick, Amy K.
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                   Roberta L.
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; FEATURE:
; OTHER INFORMATION:
US-09-919-901-14
                                                                                            ; OTHER INFORMATION: : US-09-919-901-21
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                                                                                                                                                                                                                                  SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21, Application US/09919901
Publication No. US20030082518A1
    Matches
                     Query Match
Best Local Similarity
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APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

ITITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REPERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/09/919,901

CURRENT FILING DATE: 2001-08-02

PRIOR APPLICATION NUMBER: 09/263,933

PRIOR FILING DATE: 1999-02-08

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR PILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity
                                                                                                                                   LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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TYPE: PRT
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  202; Conservative
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100.0%; Score 1032; DB 10; 100.0%; Pred. No. 1.5e-99; tive 0; Mismatches 0;
Indels
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CURRENT APPLICATION NUMBER: US/09/837,306

CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR FILING DATE: 2000-04-17
NUMBER OF SEQ ID NOS: 428
SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 354
LENGTH: 286
TYPE: PRT
Sequence 7, Application US/10191966
Publication No. US20030175692A1
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
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APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROKKEY, KRISTIN L.
APPLICANT: HOET, RENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 1032; DB 11
Best Local Similarity 100.0%; Pred. No. 1.5e-99;
Matches 202; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Unknown Organism: pCES5
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APPLICANT: Potts, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/10/191,966

CURRENT FILING DATE: 2002-07-10

PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR FILING DATE: 1999-03-08

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 14
                                                                                                                                                                      ; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-14
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                                                                                  Query Match
Best Local S
Matches 202
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CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: US/09/263,933
SOFTWARE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/10191966 Publication No. US20030175692A1 GENERAL INFORMATION:
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Best Local Similarity
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OTHER INFORMATION:
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                    Local Similarity
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  HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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                                                                               100.0%; Score 1032; DB 14; ilarity 100.0%; Pred. No. 1.5e-99; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1.5e-99;
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APPLICANT: Potts, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/10/191,966

CURRENT FILING DATE: 2002-07-10

PRIOR APPLICATION NUMBER: US/99/263,933

PRIOR FILING DATE: 1999-03-08

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn Ver. 2.0

LENGTH: 286
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US-10-045-674-523
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                                                                                                           Sequence 523, Application US/10045674 Publication No. US20030232333A1 GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT:
                                  APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROOKEY, KRISTIN L.
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ORGANISM: Artificial Sequence
FEATURE:
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HOET, RENE HOOGENBOOM,
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; OTHER INFORMATION: Description of Artificial Sequence: Vector ; OTHER INFORMATION: protein sequence US-10-045-674-523
                                                                                                                                                                ; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-416-708A-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-416-708A-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 73, Application US/10416708A; Publication No. US20040161753A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       SEQ ID NO 73
LENGTH: 286
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LENGTH: 286
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Best Local Similarity
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                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: CRÉATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING FILE OF INVENTION: SPECIFICITIES FILE REFERENCE: 37779-0004 CURRENT APPLICATION NUMBER: US/10/416,708A CURRENT FILING DATE: 2004-01-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wise, John G. APPLICANT: Fromknecht, Katja
                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 89
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                 Conservative
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                                                                            100.0%; Score 1032; DB 16; 100.0%; Pred. No. 1.5e-99; tive 0; Mismatches 0;
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Sequence 9, Application US/09919901
Publication No. US20030082518A1
GENERAL INFORMATION:
APPLICANT: Pottes, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
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SEQ ID NO 2
LENGTH: 2307
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Best Local (
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TITLE OF INVENTION: OP INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/09/919,901

CURRENT ELLING DATE: 2001-08-02

PRIOR APPLICATION NUMBER: 09/263,933

PRIOR FILLING DATE: 1999-02-08

PRIOR FILLING DATE: 1999-08-05

PRIOR FILLING DATE: 1998-08-05

NUMBER: 09/129,611

PRIOR FILLING DATE: 1998-08-05

NUMBER: 09/55
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APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
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Local Similarity 100.0%; P
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Pred. No. 2.6e-98;
0; Mismatches 0;
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; LENGTH: 2307
; TYPE: PRT
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PRIOR APPLICATION NUMBER: 09/263,933

PRIOR FILING DATE: 1999-02-08

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                          Query Match 100.0%; Score 1032; DB 10; Best Local Similarity 100.0%; Pred. No. 2.6e-98; Matches 202; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 16
LENGTH: 2307
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Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: POTTS, KAYEN E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: PATICK, AMY K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/09/919,901

CURRENT FILING DATE: 2001-08-02

PRIOR APPLICATION NUMBER: 09/263,933

PRIOR APPLICATION NUMBER: 09/263,933

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOPTWARE: Patentin Ver. 2.0
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Best Local Similarity 100.0%; Pred. No. 2.6e-98;
                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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61 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
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No. US20030082518A1
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CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
I PRIOR FILING DATE: 1998-08-05
I NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 2307
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US-10-191-966-9
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US-10-191-966-2
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                                                                                                                                                                                     Sequence 9, Application US/10191966
Publication No. US20030175692A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/10191966
Publication No. US20030175692A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 202;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILLING DATE: 2002-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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PRIOR APPLICATION NUMBER: US/09/263,933

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Search completed: June 10, Job time : 67.6736 secs
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SEQ ID NO 9
LENGTH: 2307
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 202; Conservative
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PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: :
                                                            2225
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                                                            QLIDWMEADKVAGPLLRSALPA 2246
                                                                               QLIDWMEADKVAGPLLRSALPA 202
                                                                                                                        KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 2224
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2005 Compugen Ltd.
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1144.220 Million cell updates/sec
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11 14 10 10 10 10 10 10 11 11 11 11 11 11 11	Result
975 975 975 975 975 975 975 975	Score
1000.0 1000.0 1000.0 1000.0	
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Sequence 2, Appli Sequence 7, Appli Sequence 14, Appl Sequence 21, Appl Sequence 354, Appl Sequence 7, Appli Sequence 14, Appl Sequence 21, Appl Sequence 23, Appl Sequence 73, Appl Sequence 2, Appli	Description

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US-10-280-482-8 US-10-656-029-8 US-10-177-725-3 US-10-393-449-3 US-10-491-653-146 US-10-062-188-2 US-09-925-298-760	-10-877-952- -10-469-199- -10-890-675- 09-772-114-8 09-772-114-8 -10-622-088- -10-656-029- -10-877-952-	US-09-919-901-9 US-09-919-901-16 US-10-191-966-2 US-10-191-966-9 US-10-191-966-16 US-10-191-966-16 US-10-231-013-9 US-10-842-534-9 US-10-842-534-9 US-10-872-114-6 US-09-772-114-6 US-09-772-114-7 US-09-772-114-7 US-09-772-114-7 US-09-772-114-7 US-09-772-114-7 US-09-772-114-7 US-10-866-668-5 US-10-280-482-4 US-10-877-952-71
9 2 H 3 3 8 8	9 15, 22, 28, 20, 21, 20, 20, 20, 20, 20, 20, 20, 20, 20, 20	16, 16, 16, 17, 16, 17, 18, 18, 18, 18, 18, 18, 18, 18, 18, 18

; Sequence 2, Application US/10668778 ; Publication No. US20040038317A1 ; GENERAL INFORMATION:

Robert F.

US-10-668-778-2

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APPLICANT: Her, Jeng-Horng
APPLICANT: KaloBlos, Inc.
FITLE OF INVENTION: Interaction-Activated Proteins
FILE REFERENCE: 021167-000700US
CURRENT APPLICATION NUMBER: US/10/668,778
CURRENT FILING DATE: 2003-09-22
PRIOR APPLICATION NUMBER: US/09/526,106
PRIOR FILING DATE: 2000-03-15
PRIOR FILING DATE: 2000-03-15
PRIOR FILING DATE: 1999-03-15
PRIOR APPLICATION NUMBER: US 60/124,339
PRIOR FILING DATE: 1999-03-15
PRIOR APPLICATION NUMBER: US 60/135,926
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 2000-01-13
NUMBER: US 60/175,968
PRIOR FILING DATE: 2000-01-13
NUMBER: US 50/175,968
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; TYPE: PRT
; ORGANISM: Escherichia coli
; FEATURE:
; OTHER INFORMATION: TEM-1 beta-lactamase
US-10-668-778-2
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SEQ ID NO 2
Query Match 100.0%; Score 975; DB 1: Best Local Similarity 100.0%; Pred. No. 9e-95; Matches 190; Conservative 0; Mismatches
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                                                        DB 15;
                                                        Length 263;
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US-09-919-901-14
Sequence 14, Application US/09919901
Publication No. US20030082518A1
GENERAL INFORMATION:
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US-09-919-901-7
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; OTHER INFORMATION:
US-09-919-901-7
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LENGTH: 286
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Best Local :
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APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.

ITILE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
APPLICANT: Potts, Karen E. APPLICANT: Jackson, Robert APPLICANT: Patick, Amy K.
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Local Similarity 100.0%;
es 190; Conservative 0
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Jackson, Roberta L. Patick, Amy K.
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Pred. No. 1e-94;
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APPLICANT: Potts, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/09/919,901

CURRENT FILING DATE: 2001-08-02

PRIOR APPLICATION NUMBER: 09/233,933

PRIOR FILING DATE: 1999-02-08

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0
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; OTHER INFORMATION:
US-09-919-901-14
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                                                                                            ; OTHER INFORMATION: : US-09-919-901-21
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SEQ ID NO 14
LENGTH: 286
TYPE: PRT
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Matches
                        Query Match
Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR PILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR PILING DATE: 1998-08-05
NUMBER: 09 SEQ ID NOS: 33
                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
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  Conservative
100.0%; Score 975; DB 1
100.0%; Pred. No. 1e-94;
tive 0; Mismatches
                                           DB 10;
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                       Sequence 7, Application US/10191966
Publication No. US20030175692A1
GENERAL INFORMATION:
APPLICANT: Pottes, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
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CURRENT APPLICATION NUMBER: US/09/837,306

CURRENT FILING DATE: 2001-09-24

PRIOR APPLICATION NUMBER: 60/198,069

PRIOR FILING DATE: 2000-04-17

NUMBER OF SEQ ID NOS: 428

SOFTWARE: PATENTING LATE: 2001-09-21

SEQ ID NO 354

LENGTH: 286

TYPE: PRT
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Best Local Similarity 100.0%;
Matches 190; Conservative 0
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APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROOKEY, KRISTIN L.
APPLICANT: HOET, RENE
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
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D: US20040029113A1
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Pred. No. 1e-94;
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APPLICANT: Potts, Karen B.

APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/10/191,966

CURRENT FILING DATE: 2002-07-10

PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOPTWARE: Patentin Ver. 2.0

SEQ ID NO 14

TENTUTU: 706
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CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
                                                                              Best Loc
Matches
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                                                                                                                     Query Match
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                                                                                                                                                                                     OTHER INFORMATION:
                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
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OTHER INFORMATION:
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TYPE: PRT
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nes 190; Conserv
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                                                                              100.0%; Score 975; DB 14; ilarity 100.0%; Pred. No. 1e-94; Conservative 0; Mismatches 0;
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APPLICANT: Potts, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/10/191,966

CURRENT FILING DATE: 2002-07-10

PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR FILING DATE: 1999-03-08

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 21

LENGTH: 7056
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APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROCKEY, KRISTIN L.
APPLICANT: HOET, RENE
APPLICANT: HOGGENBOOM, HENDRICU
                                                                                                                           Sequence 523, Applic Publication No. US20 GENERAL INFORMATION:
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Best Local
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OTHER INFORMATION: :
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TYPE: PRT
ORGANISM: Artificial Sequence
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Local Similarity 100.0%;
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QLIDWMEADK 213
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    HOOGENBOOM, HENDRICUS R. J.
                                                                                                                                               Application US/10045674 o. US20030232333A1
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Pred. No. 1e-94;
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                                                                                                                                              ; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-416-708A-73
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US-10-416-708A-73
                                                                                                                                                                                                                                                                        TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING TITLE OF INVENTION: SPECIFICITIES
FILE REFERENCE: 37779-0004
CURRENT FILING DATE: 2004-01-28
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.2
SEQ ID NO 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 73, Application US/10416708A publication No. US20040161753A1 GENERAL INFORMATION:
APPLICANT: Wise, John G.
APPLICANT: Fromknecht, Katja
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 190; Conservative
                                                                 Query Match
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                                                             Matches
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CURRENT APPLICATION NUMBER: US/10/045,674
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
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TYPE: PRT
ORGANISM: Artificial Sequence
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TYPE: PRT
ORGANIEM: Artificial Sequence
PEATURE:
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100.0%; Pred. No. 1e-94;
tive 0; Mismatches
                                                        100.0%; Score 975; DB 1
100.0%; Pred. No. 1e-94;
tive 0; Mismatches
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HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 83

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CURRENT APPLICATION UNMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/25,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOPTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2
LENGTH: 2307
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US-09-919-901-9
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                  Sequence 9, Application US/09919901
Publication No. US20030082518A1
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
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Publication No. US20030082518A1
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
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Sequence 16, Application US/09919901

; Sequence 16, Application US/09919901

; Publication No. US20030082518A1

; GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A

; CURRENT APPLICATION NUMBER: US/09/919,901

; CURRENT APPLICATION NUMBER: 09/263,933

; PRIOR APPLICATION NUMBER: 09/263,933

; PRIOR APPLICATION NUMBER: 09/29,611

; PRIOR APPLICATION NUMBER: 09/29,611

; PRIOR APPLICATION NUMBER: 09/29,611

; PRIOR APPLICATION STATE: 1998-08-05

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: Patentin Ver. 2.0
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PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 2307
TYPE: PRT
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                                                                                                                                                                                                                                                                                                       SEQ ID NO 16
LENGTH: 2307
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                  Query Match 100.0%; Score 975; DB 10; Best Local Similarity 100.0%; Pred. No. 1.8e-93; Matches 190; Conservative 0; Mismatches 0;
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61 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                   1 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60
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100.0%; Pred. No. 1.8e-93;
htive 0; Mismatches 0;
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RESULT 15
US-10-191-966-9
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US-10-191-966-2
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                                                                                                                                                                            Sequence 9, Application US/10191966
Publication No. US20030175692A1
GENERAL INFORMATION:
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SEQ ID NO 2
LENGTH: 2307
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APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
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CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
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APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QLIDWMEADK 190
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Pred. No. 1.8e-93;
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PRIOR APPLICATION NUMBER: US/09/263,933

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                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 9
LENGTH: 2307
TYPE: PRT
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Best Local
                                                                                                                                                                                                                                                                          Matches 190; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                          Local Similarity
2225
                                                                                                                                     2105
                                                                                                                                                                                                    2045 HPETLVKVKDABDQLGARVGYIBLDLNSGKILESFRPEERFPM%STFKVLLCGAVLSRID
                                                                                         121 KELTAFILHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 180
                                181
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                                                                                                                                                                                                                         1 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60
                                                                                                                                    AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 2164
QLIDWMEADK 2234
                         QLIDWMEADK 190
                                                                   KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 2224
                                                                                                                                                                                                                                                                        100.0%; Score 975; DB 14; 100.0%; Pred. No. 1.8e-93;
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2104

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Search completed: June 10, 2005, 11:09:06 Job time : 64.6534 secs

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No.
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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Copyright (c) 1993 - 2005 Compugen Ltd.
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/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
                                                                                                                                                                                                                                                       DB
US-09-919-901-14
US-09-919-901-21
US-09-937-306-354
US-10-191-966-7
US-10-191-966-14
US-10-191-966-21
US-10-045-674-523
US-10-416-708A-73
US-09-919-901-2
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US-09-919-901-7
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                                                                                                                                                                                                                                                       Description
               Sequence 2, Appli
Sequence 7, Appli
Sequence 14, Appli
Sequence 21, Appli
Sequence 354, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 21, Appli
Sequence 23, Appli
Sequence 523, Appli
Sequence 73, Appli
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US-10-668-778-2

Sequence 2, Application US/10668778; Publication No. US20040038317A1; GENERAL INFORMATION:

APPLICANT: Balint, Robert F. APPLICANT: Her, Jeng-Horng APPLICANT: KaloBios, Inc.

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APPLICANT: Her, Jeng-Horng
APPLICANT: KaloBios, Inc.
TITLE OF INVENTION: Interaction-Activated Proteins
FILE REFERENCE: 021167-000700US
CURRENT APPLICATION NUMBER: US/10/668,778
CURRENT APPLICATION NUMBER: US/09/526,106
PRIOR APPLICATION NUMBER: US/09/526,106
PRIOR FILING DATE: 2000-03-15
PRIOR PELLING DATE: 1900-03-15
PRIOR APPLICATION NUMBER: US 60/124,339
PRIOR PELLING DATE: 1999-03-15
PRIOR APPLICATION NUMBER: US 60/135,926
PRIOR APPLICATION NUMBER: US 60/135,926
PRIOR APPLICATION NUMBER: US 60/175,968
PRIOR APPLICATION NUMBER: US 60/175,968
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 60/175,968
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 60/175,968
PRIOR FILING DATE: 1990-05-25
PRIOR FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                  ; LENGTH: 263
; TYPE: PRT
; ORGANISM: Escherichia coli
; FEATURE:
; CTHER INFORMATION: TEM-1 beta-lactamase
US-10-668-778-2
   Query Match 100.0%; Score 925; DB 15; Best Local Similarity 100.0%; Pred. No. 2.1e-90; Matches 181; Conservative 0; Mismatches 0;
181;
                                                                        DB 15;
                                                                    Length 263;
          Indels
          <u>,</u>
          Gaps
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APPLICANT: Jockson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

APPLICANT: Patick, Amy K.

APPLICANT: Potis, Company Compan
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; OTHER INFORMATION:
US-09-919-901-7
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US-09-919-901-7
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                                                                                                   Sequence 14, Application US/09919901 Publication No. US20030082518A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
   APPLICANT: Potts, Karen E. APPLICANT: Jackson, Rober APPLICANT: Patick, Amy K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 143
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Jackson, Roberta L.
Patick, Amy K.
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Pred. No. 2.4e-90;
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RESULT 4
US-09-919-901-21
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                                                                                                                    ; OTHER INFORMATION: : US-09-919-901-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: US-09-919-901-14
Query Match
Best Local Similarity 100.
181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21, Application US/09919901 Publication No. US20030082518A1 GENERAL INFORMATION:
                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 14
SEQ ID NO 14
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Best Local Similarity
                                                                                                                                                                                                                                                                                          APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT FAPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR PILING DATE: 1998-08-05
RIGHT FILING DATE: 1998-08-05
RUMBER OF SEO ID NOS: 33
RUMBER OF SEO ID NOS: 33
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CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
CURRENT FILING DATE: 2001-08-02
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PRIOR FILING DATE: 1999-02-08
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TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                 FEATURE:
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                       100.0%; Score 925; DB 10; 100.0%; Pred. No. 2.4e-90; tive 0; Mismatches 0;
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1 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60

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FILE REPERENCE: DYAX/002
CURRENT APPLICATION NUMBER: US/09/837,306
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR FILING DATE: 2000-04-17
NUMBER OF SEQ ID NOS: 428
SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 354
LENGTH: 286
TYPE: PRT
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Sequence 7, Application US/10191966
Publication No. US20030175692A1
GENERAL INFORMATION:
APPLICANT: Pottes, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 925; DB 11; Best Local Similarity 100.0%; Pred. No. 2.4e-90; Matches 181; Conservative 0; Mismatches 0;
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APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI HORACIO G.
APPLICANT: NASTRI HORACIO G.
APPLICANT: ROOKBY, KRISTIN L.
APPLICANT: HOET, RENB
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC
TITLE OF INVENTION: DACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A
TITLE OF INVENTION: DIVERSE FAMILY OF PEPTIDES, POLYPEPTIDES OR PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE: OTHER INFORMATION: Description of Unknown Organism: pCES5
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APPLICANT: Potts, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/10/191,966

CURRENT FILING DATE: 2002-07-10

PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR FILING DATE: 1999-03-08

PRIOR FILING DATE: 1999-03-08

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR PILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 14
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CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/10191966 Publication No. US20030175692A1 GENERAL INFORMATION:
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LENGTH: 286
                                                                                        Matches
                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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                        HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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                                                                                 100.0%; Score 925; DB 14; ilarity 100.0%; Pred. No. 2.4e-90; Conservative 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/99/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 286
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                                                                                                                Sequence 523, Application No. US20 GENERAL INFORMATION:
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Best Local S
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REPERENCE: 0125-0005A
                                APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: NASKRI, KRISTIN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                                                                                                                              KELTAFLHNMGDHVTRLDRWEPBLNEAIPNDERDTTMPVAMATTLRKLLIGELLTLASRQ 180
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                  HOET,
HOOGENBOOM,
                                                                                                                                                    Application US/10045674
                                                                                                                                    US20030232333A1
                    RENE
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  HENDRICUS
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TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Vector pCES5;
OTHER INFORMATION: protein sequence
US-10-045-674-523
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US-10-416-708A-73
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CURRENT APPLICATION NUMBER: US/10/045,674
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR PILING DATE: 2001-04-17
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
                                                                                                                                                                                                                                                                                                                                                              Sequence 73, Application US/10416708A

Publication No. US20040161753A1

GENERAL INFORMATION:

APPLICANT: Wise, John G.

APPLICANT: Fromknecht, Katja

TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING

TITLE OF INVENTION: SPECIFICITIES

FILE REFERENCE: 37779-0004

CURRENT APPLICATION NUMBER: US/10/416,708A

CURRENT APPLICATION NUMBER: US/10/416,708A

CURRENT FILING DATE: 2004-01-28

NUMBER OF SEQ ID NOS: 89

SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                SEQ ID NO 73
LENGTH: 286
TYPE: PRT
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SEQ ID NO 523
LENGTH: 286
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Best Local Similarity
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                                                                                                                                                                                                                      FEATURE: OTHER INFORMATION: Synthetic Construct
                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 Q 204
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                       1 HPETLVXVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60
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HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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                                                                                                  Conservative
                                                                                            100.0%; Score 925; DB 16; 100.0%; Pred. No. 2.4e-90; tive 0; Mismatches 0;
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100.0%; Pred. No. 2.4e-90;
tive 0; Mismatches 0;
                                                                                                                                           Length 286;
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RESULT 12
US-09-919-901-9
; Sequence 9, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
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; OTHER INFORMATION:
US-09-919-901-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: CONTRIBUTORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REPERENCE: 0125-0005A
CURRENT FILING DATE: 001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 2307
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APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
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ORGANISM: Artificial Sequence
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PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
LENGTH: 2307
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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PRIOR APPLICATION NUMBER: 09/263,933
PRIOR PILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR PILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 2307
TYPE: PRI
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                                                                                                                                         Matches
                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
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OTHER INFORMATION: :
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                                                                                                                                       181;
61 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
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                                                                                                                                     100.0%; Score 925; DB 10; illarity 100.0%; Pred. No. 4.2e-89; Conservative 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/99/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
PRIOR
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US-10-191-966-9
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Publication No. US20030175692A1
GENERAL INFORMATION:
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Best Local Similarity
                      APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REPERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
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APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
PRIOR APPLICATION NUMBER: US/09/263,933
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Pred. No. 4.2e-89;
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SEQ ID NO 9
LENGTH: 2307
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                            2165
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2225 Q 2225
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                                    181 Q 181
                                                                                                  121 KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 180
                                                                                                                                                                                  61 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
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                                                                            KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 2224
                                                                                                                                                      AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 2164
                                                                                                                                                                                                                                                                                                           100.0%; Score 925; DB 14; 100.0%; Pred. No. 4.2e-89; tive 0; Mismatches 0;
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Search completed: June 10, Job time : 61.6383 secs 2005, 11:09:04

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                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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| (cgn2 6/ptodata/2/pubpaa/PCT NEW PUB.pep:*
| (cgn2 6/ptodata/2/pubpaa/US06 NEW PUB.pep:*
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/ CGM2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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/ CGM2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/ CGM2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
/ CGM2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
/ CGM2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
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/ CGM2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
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US-10-062-188-2 US-09-925-298-760	10-060-100-	-10-393-449-	US-10-177-725-3	US-10-491-653-146	US-10-656-029-8	US-10-280-482-8	US-09-772-114-9	7-95	US-10-656-029-6	US-10-622-088-114	US-10-280-482-6	US-09-772-114-8	-10-890-675-	US-10-469-199-2	US-10-877-952-18	-10	US-10-877-952-26	US-10-656-029-4	US-10-280-482-4	US-10-016-668-5	US-09-772-114-7	US-10-656-029-2	US-10-280-482-2	US-09-772-114-6	US-10-477-044-1	-10-	-10-	-10-231-013-	-10-191-966-	US-10-191-966-9	US-10-191-966-2	-919-901-	US-09-919-901-9
Sequence 2, Appri Sequence 760, App	٠.	ω	ω •	146	8	e 8,	9, 1	Sequence 154, App		11,	e 6,	Sequence 8, Appli	N	N	18,	71,	26,	4.	4	e 5,	7,	Ņ	e 2	6	Sequence 1, Appli	N	9	e 9,	e 16,	e 9,	2	Ó	٠

US-10-668-778-2

Sequence 2, Application US/10668778 Publication No. US20040038317A1 GENERAL INFORMATION:

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APPLICANT: Halint, Robert F.

APPLICANT: Her, Jeng-Horng
APPLICANT: Her, Jeng-Horng
APPLICANT: KaloBios, Inc.
TITLE OF INVENTION: Interaction-Activated Proteins
FILE REFERENCE: 021167-000700US
CURRENT PILING DATE: 2003-09-22
PRIOR APPLICATION NUMBER: US/09/526,106
PRIOR APPLICATION NUMBER: US/09/526,106
PRIOR FILING DATE: 1999-03-15
PRIOR FILING DATE: 1999-03-15
PRIOR APPLICATION NUMBER: US 60/124,339
PRIOR FILING DATE: 1999-03-15
PRIOR APPLICATION NUMBER: US 60/135,926
PRIOR APPLICATION NUMBER: US 60/175,968
PRIOR FILING DATE: 1990-03-25
PRIOR APPLICATION NUMBER: US 60/175,968
PRIOR FILING DATE: 2000-01-13
INMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 263
TYPE: PRT
ORGANISM: Escherichia coli
FEATURE:
OTHER INFORMATION: TEM-1 beta-lactamase
US-10-668-778-2
Query Match
Dest Local Similarity 100.0%; Pred. No. 1.3e-87;
Matches 172; Conservative 0; Mismatches 0; Gaps
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Length

286;

Indels

0;

Gaps

0

143

83

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TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR FILING DATE: 1999-03-08
PRIOR FILING DATE: 1999-08-05
NUMBER: 09 SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
IFROTERS
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; Sequence 14, Application US/09919901
; Publication No. US20030082518A1
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US-09-919-901-7
                                                                                                          GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 01055-0005A
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Publication No. US20030082518A1
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Best Local :
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Local Similarity 100.0%;
Les 172; Conservative 0
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Pred. No. 1.4e-87;
0; Mismatches 0;
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Best Local Similarity 100.
Matches 172; Conservative
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Publication No. US20030082518A1
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LENGTH: 286
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APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILLING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILLING DATE: 1999-02-08
PRIOR FILLING DATE: 1999-02-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: :
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                               61 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
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                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 885; DB 10; 100.0%; Pred. No. 1.4e-87; tive 0; Mismatches 0;
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Length 286;

Indels

0;

Gaps

US-09-837-306-354

Sequence 354, Application US/09837306 Publication No. US20040029113A1

GENERAL INFORMATION:

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; PEATURE:
; OTHER INFORMATION: Description of Unknown Organism: pCES5
US-09-837-306-354
                                                                       GTHER INFORMATION: US-10-191-966-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC TITLE OF INVENTION: PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A TITLE OF INVENTION: DIVERSE FAMILY OF PEPTIDES, POLYPEPTIDES OR PROTEINS FILL REFERENCE: DYAX/002

CURRENT APPLICATION NUMBER: US/09/837,306

CURRENT FILING DATE: 2001-09-24

PRIOR APPLICATION NUMBER: 60/198,069

PRIOR PILING DATE: 2000-04-17

NUMBER OF SEQ ID NOS: 428

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 354

LENGTH: 286
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Query Match
Best Local Similarity
                                                                                                                                                                                                                  SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROOKEY, KRISTIN L.
APPLICANT: HOET, RENE
                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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100.0%;
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Score 885; DB 14;
Pred. No. 1.4e-87;
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                      Length 286;
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PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR FILING DATE: 1998-08-05
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOPTWARE: PATENTIN Ver. 2.0
SEQ ID NO 14
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: TIPOLOGY
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                                                                                                                                                                                               Sequence 21, Application US/10191966
Publication No. US20030175692A1
GENERAL INFORMATION:
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Publication No.
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Best Local :
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APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Pattck, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INFIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
APPLICANT: Potts, Karen E.
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/10/191,966
PRIOR APPLICATION NUMBER: US/09/263,933
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to. US20030175692A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 885; DB 14; ilarity 100.0%; Pred. No. 1.4e-87; Conservative 0; Mismatches 0;
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TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTION: OF INVENTION: DISPLAYED AND/OR EXPRESS;
TITLE OF INVENTION: OF PERFIDDES, POLYPEPTIDITIVE OF INVENTION: LIBRARIES
FILE REFERENCE: DYAX/002 CIP2
CURRENT APPLICATION NUMBER: US/10/045,674
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
PRIOR FILING DATE: 2001-04-17
NUMBER: OF SEQ ID NOS: 635
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 523
LENGTH: 286
TYPE: PRT
TYPE: PRT
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; OTHER INFORMATION:
US-10-191-966-21
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Best Local Similarity 100.0%;
Matches 172; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 523, Application US/10045674 Publication No. US20030232333A1
                                                                                                                                                       Matches
                                                                                                                                                                                             Query Match
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PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LADNER, APPLICANT: COHEN, APPLICANT: NASTRI,
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                     Local Similarity nes 172; Conserv
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INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                       HPETLYKYKDAEDQLGARVGYIELDLNSGKILESFRPBERFPMMSTFKVLLCGAVLSRID 60
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ROOKEY,
                                                                HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPBERFPMMSTFKVLLCGAVLSRID
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COHEN, EDWARD H.
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                                                                                                                                                   100.0%; Score 885; DB 15; ilarity 100.0%; Pred. No. 1.4e-87; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                            Description of Artificial Sequence: Vector pCES5 protein sequence
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KRISTIN L.
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Pred. No. 1.4e-87;
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                                                                                                                                                                                             DB 15;
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                                                                                                                                                                                           Length 286;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-416-708A-73
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                                                                                                                                                                   GENERAL INFORMATION:

APPLICANT: Potts, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

APPLICANT: Patick, Amy K.

APPLICANT: PATICK, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/09/919,901

CURRENT FILING DATE: 2001-08-02

PRIOR APPLICATION NUMBER: 09/263,933

PRIOR FILING DATE: 1999-02-08

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33
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Publication No. US20040161753A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09919901 Publication No. US20030082518A1
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Best Local
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APPLICANT: Fromknecht, Katja
APPLICANT: Fromknecht, Katja
TITLE OP INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING
TITLE OP INVENTION: SPECIFICITIES
FILE REFERENCE: 37779-0004
CURRENT FAPLICATION NUMBER: US/10/416,708A
CURRENT FILLING DATE: 2004-01-28
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.2
                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0
                                                                        LENGTH: 23
TYPE: PRT
FEATURE:
OTHER INFORMATION: :
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ORGANISM: Artificial Sequence
                                                 ORGANISM: Artificial Sequence
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                                                                                                     2307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 885; DB 16; ilarity 100.0%; Pred. No. 1.4e-87; Conservative 0; Mismatches 0;
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RESULT 13
US-09-919-901-16
; Sequence 16, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; FILE REFERENCE: 0125-0005A
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CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver: 2.0
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LENGTH: 2307

TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Best Local Similarity
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APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
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APPLICANT: Potts, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/10/191,966

CURRENT FILING DATE: 2002-07-10

PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR FILING DATE: 1999-03-08

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

TENGTH- 7307
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                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 172; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOPTWARE: PatentIn Ver. 2.0
SEQ. ID NO 16
LENGTH: 2307
TYPE: PRT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                          FEATURE:
OTHER INFORMATION: :
                                                                                                                                                                                                                                                                                                                                                                LENGTH: 2307
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION:
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                                                                                                                                              2045 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLLTTIGGP 120
                                                                                                                                                                       1 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
KELTAFLHNMGDHVTRLDRWEFELNEAIFNDERDTTMFVAMATTLRKLLTGE
                                                                 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                        AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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                                                                                                                                                                                                                        100.0%; Score 885; DB 14;
100.0%; Pred. No. 2.6e-86;
ative 0; Mismatches 0;
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                                                                                                                                                                                                                            Indels
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2165 KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGE 2216

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RESULT 15

US-10-191-966-9

Sequence 9, Application US/10191966

Publication No. US20030175692A1

GENERAL INFORMATION:

APPLICANT: Patick, Amy K.

APPLICANT
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein - protein search, using sw model
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Copyright (c) 1993 - 2005 Compugen Ltd.
/ Cgm2_6/ptodata/2/pubpaa/US08_NEW_PUBCOMB.pep:*
/ Cgm2_6/ptodata/2/pubpaa/US08_NEW_PUBCOMB.pep:*
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/ Cgm2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/ Cgm2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
/ Cgm2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
/ Cgm2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

110087654 110087654	Result
770 770 770 770 770 770 770	Score
100.0 100.0 100.0 100.0 100.0 100.0	% Query Match
2308663	Query Query Match Length
15 10 10 11 14 14 15	DB
US-10-668-778-2 US-09-919-901-7 US-09-919-901-14 US-09-919-901-21 US-09-837-306-354 US-10-191-966-7 US-10-191-966-14 US-10-191-966-21 US-10-045-674-523 US-10-045-674-523 US-10-045-674-523 US-10-045-674-523 US-10-045-674-523	SUMMARIES
Sequence 2, Appli Sequence 7, Appli Sequence 14, Appl Sequence 21, Appl Sequence 354, Appl Sequence 7, Appli Sequence 14, Appli Sequence 21, Appl Sequence 523, Appli Sequence 73, Appli Sequence 73, Appli	Description

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US-09-925-298-760	US-10-062-188-2	US-10-393-449-3	US-10-177-725-3	-10-491-653-	US-10-656-029-8	US-10-280-482-8	US-09-772-114-9	US-10-877-952-154	US-10-656-029-6	US-10-622-088-114	US-10-280-482-6	US-09-772-114-8	US-10-890-675-2	US-10-469-199-2	US-10-877-952-18	-10-477-	US-10-251-385-292	US-10-877-952-71	-10-877-952	US-10-656-029-4	-10-842-534	US-10-280-482-4	US-10-231-013-9	US-10-016-668-5	US-09-772-114-7	US-10-656-029-2	US-10-280-482-2	US-09-772-114-6	-10-191-	US-10-191-966-9	-10-191-	ò	US-09-919-901-9
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ALIGNMENTS

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APPLICANT: Her, Jeng-Horng
APPLICANT: KaloBios, Inc.
TITLE OF INVENTION: Interaction-Activated Proteins
FILE REFERENCE: 021167-000700US
CURRENT APPLICATION NUMBER: US/10/668,778
CURRENT FILING DATE: 2003-09-22
PRIOR APPLICATION NUMBER: US/09/526,106
PRIOR PILING DATE: 2000-03-15
PRIOR PILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: US 60/124,339
PRIOR PILING DATE: 1999-03-15
PRIOR PILING DATE: 1999-03-15
PRIOR APPLICATION NUMBER: US 60/135,926
PRIOR PILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 60/175,968
PRIOR PILING DATE: 1990-05-25
PRIOR APPLICATION NUMBER: US 60/175,968
PRIOR FILING DATE: 000-01-13
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
                                                                                                                   ; LENGTH: 263
; TYPE: PRT
; ORGANISM: Escherichia coli
; PEATURE:
; OTHER IMPORMATION: TEM-1 beta-lactamase
US-10-668-778-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
US-10-668-778-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 2, Application US/10668778 ; Publication No. US20040038317A1 ; GENERAL INFORMATION:
Query Match 100.0%; Score 770; DB 15; Best Local Similarity 100.0%; Pred. No. 2.7e-77; Matches 149; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Balint, Robert F. APPLICANT: Her, Jeng-Horng APPLICANT: KaloBios, Inc.
                                                         Length 263;
         Indels
         0
         Gaps
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APPLICANT: Potts, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/09/919,901

CURRENT FILING DATE: 2001-08-02

PRIOR APPLICATION NUMBER: 09/263,933

PRIOR APPLICATION NUMBER: 09/263,933

PRIOR APPLICATION NUMBER: 09/29,611

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR PRIOR APPLICATION NUMBER: 09/129,611
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; Sequence 14, Application US/09919901 ; Publication No. US20030082518A1
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                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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Best Local S
                   APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 0901-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR FILING DATE: 1999-02-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 149; Conserv
APPLICATION NUMBER: 09/129,611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KELTAFLHNMGDHVTRLDRWEPELNEAIP 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-919-901-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 21
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21, Application US/09919901 Publication No. US20030082518A1
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NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
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Best Local 9
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CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
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APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Potts, Karen E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0
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OTHER INFORMATION: :
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                        HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60
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                                                                                 KELTAFLHNMGDHVTRLDRWEPELNEAIP 172
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-09-837-306-354

Application US/09837306 US20040029113A1

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APPLICANT: Potts, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/10/191,966

CURRENT FILING DATE: 2002-07-10

PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR FILING DATE: 1999-03-08

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR APPLICATION NUMBER: 09/129,611
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ORDANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: pCES5
US-09-837-306-354
                                                                                       ; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-7
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CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR FILING DATE: 2000-04-17
NUMBER OF SEQ ID NOS: 428
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 354
LENGTH: 286
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Query Match
Best Local Similarity
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APPLICANT: COHEN, EDWARD H.
APPLICANT: WASTRI, HORACIO G.
APPLICANT: ROOKEY, KRISTIN L.
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                                                                                                                                                                       LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
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100.0%;
Score 770; DB 14;
Pred. No. 3e-77;
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                           Length 286
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US-10-191-966-14
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                                                                                                                                                                                                                           Sequence 21, Application US/10191966 Publication No. US20030175692A1 GENERAL INFORMATION:
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PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 14
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Publication No.
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APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT PELLICATION NUMBER: US/10/191,966
CURRENT PILLING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
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APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
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TYPE: PRT
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No. US20030175692A1
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PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05

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                                                                                                                                                                                                                                                                                               SEQ ID NO 523
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
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LENGTH: 286
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Best Local Similarity
                                                                                                                                          Matches
                                                                                                                                                                               Query Match
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APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.

TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
TITLE OF INVENTION: LIBRARIES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION: LIBRARIES,
FILE REFERENCE: DYAX/002 CIP2
CURRENT APPLICATION NUMBER: US/10/045,674
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR PILING DATE: 2000-04-17
RIOR APPLICATION NUMBER: 09/837,306
PRIOR PILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
SOFTMARE: PATENTIN Ver. 2.1
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APPLICANT: COHEN, EDWARD H.
APPLICANT: WASTRI, HORACIO G.
APPLICANT: ROOKEY, KRISTIN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Vector pCESS OTHER INFORMATION: protein sequence
                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                             Local Similarity
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                                                                                HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60
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AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                             HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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                                                                                                                                                             Score 770; DB 1
Pred. No. 3e-77;
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Publication No. US20030082518A1
                                                                                                                          SEQ ID NO 2
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                                                                                                                                                                APPLICANT: POLLS, KATEN E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT PAPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1998-08-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEO ID NOS: 33
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APPLICANT: Fromknecht, Katja
APPLICANT: Fromknecht, Katja
TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING
TITLE OF INVENTION: SPECIFICITIES
FILE REFERENCE: 37779-0004
CURRENT APPLICATION NUMBER: US/10/416,708A
CURRENT FILING DATE: 2004-01-28
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                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
                                             ORGANISM: Artificial Sequence
                                                                           TYPE: PRT
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100.0%; Pred. No. 3e-77;
tive 0; Mismatches
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RESULT 13
US-09-919-901-16
J Sequence 16, Application US/09919901
Publication No. US20030082518A1
GENERAL INFORMATION:
GENERAL INFORMATION:
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US-09-919-901-9
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Publication No. US20030082518A1
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LENGTH: 2307
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APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REPERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
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APPLICANT: POTTS, Karen B.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OP INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OP INVENTION: OP INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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Pred. No. 5e-76;
D; Mismatches 0;
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LENGTH: 2307
TYPE: PRT
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Best Local S
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   KELTAFLHNMGDHVTRLDRWEPELNEAIP 149
                                                                                                                                                                                                         Conservative
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APPLICANT: Potts, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/10/191,966

CURRENT FILING DATE: 2002-07-10

PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR FILING DATE: 1999-03-08

PRIOR FILING DATE: 1999-03-08

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR APPLICATION VUMBER: 09/129,611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/10191966 Publication No. US20030175692A1 GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence FEATURE:
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                                                    61 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
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AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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2165 KELTAFLHNMGDHVTRLDRWEPELNEAIP 2193

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RESULT 15

US-10-191-866-9

Sequence 9, Application US/10191966

Publication No. US2000175692A1

GENERAL INCORMATION:

APPLICANT: Potte, Karen E.

APPLICANT: Potte, Karen
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Database :
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Maximum Match 100%
Listing first 45 summaries
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(ggn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

(ggn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

(ggn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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/ Cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1348 1348 1348 1348 1348 1348 1348 1348	Score
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US-10-668-778-2 US-09-919-901-7 US-09-919-901-21 US-09-919-901-21 US-09-837-306-354 US-10-191-966-7 US-10-191-966-14 US-10-191-966-21 US-10-045-674-523 US-10-045-674-523 US-10-919-901-2	SUMMARIES
Sequence 2, Appli Sequence 7, Appli Sequence 11, Appl Sequence 21, Appl Sequence 354, Appli Sequence 7, Appli Sequence 14, Appli Sequence 21, Appl Sequence 53, Appli Sequence 73, Appli Sequence 73, Appli	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13
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US-10-062-188-3	US-10-062-188-2	-10-491-	US-10-393-449-3	US-10-177-725-3	US-10-656-029-8	US-10-280-482-8	US-09-772-114-9	US-10-877-952-154	US-10-656-029-6	US-10-622-088-114	US-10-280-482-6	US-09-772-114-8	US-10-890-675-2	US-10-469-199-2	US-10-877-952-18	US-10-877-952-71	US-10-877-952-26	US-10-656-029-4	US-10-280-482-4	US-10-016-668-5	US-09-772-114-7	US-10-656-029-2	US-10-280-482-2	US-09-772-114-6	US-10-477-044-1	US-10-251-385-292	US-10-842-534-9	013	966	-10-191-	US-10-191-966-2	US-09-919-901-16
		14		Sequence 3, Appli	8,	8,	യ	Sequence 154, App		Sequence 114, App	Sequence 6, Appli		Sequence 2, Appli	2	Sequence 18, Appl	Sequence 71, Appl	26		4	(D	,7	2,	e 2	Sequence 6, Appli	Sequence 1, Appli	Sequence 292, App	Sequence 9, Appli					Sequence 16, Appl

US-10-668-778-2

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Sequence 2, Application US/10668778

Publication No. US20040038317A1

REGINERAL INFORMATION:

APPLICANT: HeI, Jeng-Horng

APPLICANT: HeI, Jeng-Horng

APPLICANT: KALOBIOS, Inc.

TITLE OF INVENTION: Interaction-Activated Proteins

FILE REFERENCE: 021167-000700US

CURRENT APPLICATION NUMBER: US/10/668,778

CURRENT FILING DATE: 2003-09-22

PRIOR APPLICATION NUMBER: US/99/526,106

PRIOR PILING DATE: 2000-03-15

PRIOR PILING DATE: 1999-03-15

PRIOR APPLICATION NUMBER: US 60/124,339

PRIOR FILING DATE: 1999-05-25

PRIOR APPLICATION NUMBER: US 60/124,339

PRIOR FILING DATE: 1999-05-25

PRIOR APPLICATION NUMBER: US 60/124,339

PRIOR FILING DATE: 1999-05-25

PRIOR FILING DATE: 2000-01-13

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                       ; OTHER INFORMATION: TEM-1 beta-lactamase US-10-668-778-2
                                                                                                                                                                                                                                                                                                                                  SOFTWARE: SEQ ID NO 2
Query Match 100.0%; Score 1348; DB 15; Best Local Similarity 100.0%; Pred. No. 2.2e-125; Matches 263; Conservative 0; Mismatches 0;
                                                                                                                                                                                                 LENGTH: 263
TYPE: PRT
ORGANISM: Escherichia coli
FEATURE:
                                                                       DB 15; Length 263;
             Indels
          0;
          Gaps
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PRIOR APPLICATION NUMBER: 09/263,933
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR FILING DATE: 1999-02-08
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH. 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Potts, Karen B.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT APPLICATION DATE: 2001-08-02
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TYPE: Artificial Sequence
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264 ŚOÁTMDERNRÓTABTGÁŚLIKHW 286
                       241 SQATMDERNROIAEIGASLIKHW 263
                                                                                                                                                                                                                                                                                                      n 100.0%; Score 1348; DB 10; Similarity 100.0%; Pred. No. 2.4e-125; 3; Conservative 0; Mismatches 0;
                          204 OLIDWEADKVAGPLLESALPÄÖN (SGAGERGSRGIIAALGPDGKPSRIVVIYTTG 240 (SQATMDERNFOTTAR) (SGAGERGSRGIIAALGPDGKPSRIVVIYTTG 263
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APPLICANT: Potts, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

ITILE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

ITILE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/09/919,901

CURRENT FILING DATE: 2001-08-02

PRIOR APPLICATION NUMBER: 09/263,933

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 21

LENGTH: 286
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APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A

CURRENT FILING DATE: 2001-08-02

PRIOR APPLICATION NUMBER: 09/263,933

PRIOR PILING DATE: 1999-02-08

PRIOR PILING DATE: 1998-08-05

PRIOR FILING DATE: 1998-08-05

NUMBER: OF SEQ ID NOS: 33

ROFTWARE: DATE: 1998-08-05

NUMBER: OF SEQ ID NOS: 33
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TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
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FILE REPERENCE: DYAX/002

CURRENT APPLICATION NUMBER: US/09/837,306

CURRENT FILING DATE: 2001-09-24

PRIOR APPLICATION NUMBER: 60/198,069

PRIOR FILING DATE: 2000-04-17

NUMBER OF SEQ ID NOS: 428

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 354

LENGTH: 286
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                                                                                                                                                                                                               Query Match 100.0%; Score 1348; DB 11; Best Local Similarity 100.0%; Pred. No. 2.4e-125; Matches 263; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROCKEY, KRISTIN L.
APPLICANT: HOET, RENE
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC
TITLE OF INVENTION: PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A
TITLE OF INVENTION: DIVERSE FAMILY OF PEPTIDES, POLYPEPTIDES OR PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 1348; DB 10; Best Local Similarity 100.0%; Pred. No. 2.4e-125;
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ORGANISM: Unknown Organism
FEATURE:
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GENERAL INFORMATION:
APPLICANT: POtts, Karen E.
APPLICANT: Jackson, Roberta
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER
TITLE OF INVENTION: OF INH
                                                                                                                          RESULT 7
US-10-191-966-14
; Sequence 14, Appl
; Publication No. U
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US-10-191-966-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local Similarity
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APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: PATICK, AMY K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER: 1998-08-05
NUMBER: 1998-08-05
NUMBER: 05/129,611
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ORGANISM: Artificial
FEATURE:
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                                                                                                                                                                                                                                                   SOATMDERNROIAEIGASLIKHW 286
                                                                                                                            Application US/10191966
Amy K.
REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
                                                                 Roberta L.
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Sequence 21, Application US/1019166

Publication No. US20030175692A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Potte, Karen E.
APPLICANT: Potte, Karen E.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT PILING DATE: 1090-03-08
CURRENT PILING DATE: 1090-03-08
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1098-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
PRIOR PLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 286
; TYPE: PRT
ORGANISM: Artificial Sequence
FEATHER:
                                                                                 ; FEATURE:
; OTHER INFORMATION:
US-10-191-966-21
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US-10-191-966-14
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    Matches
                   Query Match
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cvative 0;
100.0%; Score 1348; DB 14; 100.0%; Pred. No. 2.4e-125; tive 0; Mismatches 0;
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Pred. No. 2.4e-125;
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APPLICANT: HOET, RENE
APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 523
LENGTH: 286
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Best Local
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tch 100.0%; Score 1348; DB 15; al Similarity 100.0%; Pred. No. 2.4e-125; 263; Conservative 0; Mismatches 0;
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COHEN, EDWARD H.
NASTRI, HORACIO G.
ROOKEY, KRISTIN L.
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                                                                                                                                                                                                                                                               AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 143
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TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING; TITLE OF INVENTION: SPECIFICITIES; FILE REFERENCE: 37779-0004; CURRENT APPLICATION NUMBER: US/10/416,708A; CURRENT FILING DATE: 2004-01-28; NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.2
SEQ ID NO 73
LENGTH: 286
Type: new
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US-09-919-901-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09919901 Publication No. US20030082518A1 GENERAL INFORMATION:
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                                                                                                     APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1999-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
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ORGANISM: Artificial Sequence
FEATURE:
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Pred. No. 2.4e-125;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 9
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                 LENGTH: 2307
TYPE: PRT
ORGANISM: Artificial S
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
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                                                                                                                                                                                                                                                                                                   OTHER INFORMATION:
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                 2045 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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                                                                               61 AGQEQIGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
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                                                       AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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Conservative 0
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Pred. No. 4.6e-124;
D; Mismatches 0;
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US-09-919-901-16
; Sequence 16, Application US/09919901
; Deblication No. US20030082518A1
; Publication No. US20030082518A1
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                                                                                                                            Sequence 2, Application US/10191966 Publication No. US20030175692A1 GENERAL INFORMATION:
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APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver: 2.0
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
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OTHER INFORMATION:
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Local Similarity 100.0%;
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Pred. No. 4.6e-124;
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                                                                                                                                       ; SEQ ID NO 9
; LENGTH: 2307
; TYPE: PRT
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LENGTH: 2307
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/10191966
Publication No. US20030175692A1
                                                                                                                                                                                                              APPLICANT: PORTES, KATER E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: PARTICK, RAMY K.

APPLICANT: PARTICK, REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: COPINHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/10/191,966

CURRENT FILING DATE: 2002-07-10

PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR FILING DATE: 1999-03-08

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

NUMBER OF SEQ ID NOS: 33
Query Match
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CURRENT FILLING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0
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                                                                         OTHER INFORMATION: :
                                                                                              FEATURE:
                                                                                                                ORGANISM: Artificial Sequence
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OTHER INFORMATION:
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Similarity 100.0%;
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Pred. No. 4.6e-124;
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Best Local Similarity Matches 263; Conserve

Conservative

100.0%; Score 1348; DB 14; 100.0%; Pred. No. 4.6e-124; tive 0; Mismatches 0;

DB 14;

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Gaps

	SQATMDERNRQIAEIGASLIKHW 263	, 241 2285	유왕
240 2284	QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG 	, 181	음 성
180 2224	KELTAFLHIMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 		유왕
120 2164	AGQEQLGRRIHYSQNDLVBYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120	, 61 2105	음 성
60 2104	HPETLYKVKOAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60	2045	음 성

Search completed: June 10, 2005, 11:09:03 Job time : 89.1097 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd

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Listing first 45 summaries
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SUMMARIES

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Vector Novel h	Adr70404 Vector pa Adr70416 Vector pa	Vector	Abr43622 Cloning v Adr70422 Vector pA		Aau75551 celZ inte	Aab31173 Amino aci	Aab50898 Protein e	Aab10440 Expressio	Aab10438 Expressio	Aab10442 Expressio	Aay08529 Vector pA	Aaw18679 Secretory	Aaw16635 Beta-lact	Aar96423 Cytochrom	Aar97619 Secretory	Aar31575 Ampicilli	Aaw18680 Intracell	Aaw16634 Beta-lact	Adj67709 Escherich	Aab36692 Escherich	Aae05544 E. coli m	Description

13-JAN-2000; 2000US-0175968P. 15-MAR-2000; 2000US-00526106. 16-JAN-2001; 2001WO-US001651 WO200151629-A2

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Aab62272	Adm97749	Aam51111	Aae06922	Aay49890	Aaw48613	Aay08232	Adh11249	Aay70066	Aay70065	Aay70064	Aar52701	Aar88636	Adi46109	Ada67747	Abr55981	Abr55980	Aaw18681	Aaw16636	Aam84362
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ALIGNMENTS

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XX Ci;c Cleavage-site Region Key Cleavage-site Escherichia coli. Interaction-dependent enzyme association; IdEA system; biosensor; circularly permutated interaction-activated protein; marker protein; type A beta-lactamase; TEM-1 beta-lactamase; protein-protein interaction; therapeutic; drug screening; thioredoxin; ampicillin resistance. E. coli mature TEM-1 beta-lactamase AAE05544 standard; protein; 263 Cleavage-site Cleavage-site Region Cleavage-site Cleavage-site Active-site Cleavage-site Cleavage-site 24-SEP-2001 AAE05544; (first entry) Location/Qualifiers 27. .28 190. .191 149. .150 /note= "Break-point between alpha and /note= 'note= note= "Break-point between alpha note= "Inter-sub-domain loop" note= "Break-point between alpha note= note= note= "Break-point between alpha and omega note= "Break-point between alpha and omega fragments" . 40 .173 .204 . 39 .203 .229 "Inter-sub-domain loop" "Break-point between alpha "Break-point between alpha and omega fragments" "Break-point between alpha ₿ and and and and omega omega omega omega omega fragments" fragments" fragments" fragments" fragments" fragments"

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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC The marker protein is preferably a type A beta-lactamase, especially TEM-
CC 1 beta-lactamase of Escherichia coli. The oligopeptide is a member of a
CC proteome library selected from single chain antibody FV fragment library,
CC an antibody light chain variable region library and a peptide library,
CC displayed within thioredoxin. The IGEA systems are useful for detecting
CC and identifying interactions between intracellular as well as selecting systems are also useful in selecting with a single marker protein the
CC incorporation of multiple genetic traits in a host cell. In particular,
CC diagnostics and prognostics, as well as in high-throughput screening
CC systems for the discovery and validation of pharmaceutical targets and
CC drugs. Prior systems (e.g. E. coli Dimer Detection System) yeast two-
CC hybrid system or Selective Infective Phage System) require multiple steps
CC between interaction and phenotype, which cause severe loss of efficiency
CC between interaction and phenotype, which cause severe loss of efficiency
CC due to high false positive and false negative rates. The present system
CC dependent enzymes find use in cell-based sensors for activation or
CC dependent enzymes find use in cell-based sensors for activation or
CC dependent enzymes find use in cell-based sensors for activation or
CC dinhibition of metabolic or signal transduction pathways, in high-
CC dinhibition of metabolic or signal transduction pathways, in high-
CC dinhibition of metabolic or signal transduction of inhibitors within and
CC continued to the proteomes of cells, tissues and pathogenic organisms, and in
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Best Local Similarity
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AAB36692 standard; protein; 263 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 263 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IdEA) systems that comprise a fusion sequence that encodes for a circularly permutated, interaction-activated proteins that reassemble to form functionally reconstituted marker proteins which produce a detectable signal upon the association of two oligopeptides, or upon simultaneous association of two oligopeptides with a third oligopeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interaction-dependent enzyme association systems for detecting interactions between two or three polypeptides, especially in human therapeutics, diagnostics or prognostics, comprise circularly permutated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAD10411.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 38; Fig 2; 104pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lactamase is a product of ampicillin domains, alpha-omega and mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to new interaction-dependent enzyme association
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PANO-) PANORAMA RES
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                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                KELTAFLHNMGDHVTRLDRWEPELNEAIP 149
                                                                                                                                                                                                                                                                 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLITTIGGP 120
                                                                                                                                                                                                                                                                                                                                          HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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Pred. No. 7.8e-80;
); Mismatches 0;
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                                                                                                                                                                                               Matches
                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                              Sequence 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel fragment complementation system to identify interactions between polypeptides comprises fragment pairs having first and second members that reassemble into a marker protein which has a directly detectable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAY-1999; 99US-0135926P.
13-JAN-2000; 2000US-0175968P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interaction-activated protein; beta-lactamase; protein interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB36692;
                                                                                                                                                                                                              Local
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DB; AAC90773.
121
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                                                                                                                                                                                                              Similarity
                                                                                                                             HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                    KELTAFLHNMGDHVTRLDRWEPELNEAIP 149
                                                                                  AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLITTIGGP 120
                                                                                                                                                    HPETLYKVKDASDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60
KELTAFLHNMGDHVTRLDRWEPELNEAIP 149
                                                               AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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                                                                                                                                                                                               0,
                                                                                                                                                                                           Score 770; DB 4;
Pred. No. 7.8e-80;
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                                                                                                                                                                                               Indels
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RESULT 3 ADJ67709

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Ct terminal fragment each are derived from a marker protein and treasemble to form a functionally reconstituted marker protein. (I) is useful for selecting simultaneous incorporation of multiple genetic elements into a compound in a host. The method described is useful for identifying a compound in a host. The method described is useful for identifying a compound in a host. The method described is useful for identifying a compound in a host. The method described is useful for identifying a compound in a host. The method is useful for identifying a compound in a host. The method is useful for identifying a compound in a become oligopeptide. Binding of the first coligopeptide to the second oligopeptide. Binding of the first coligopeptide to the second oligopeptide results in the functional compound to respect to the marker protein. The method is also useful for compound in a sample; and identifying oligopeptide interactions between two different proteomes; compound identifying epitopes that bind to an immunoglobulin variable region. (I) or an expression casette (II), encoding a selectable N or C-terminal compound in a useful for identifying interactions between an extra cellular domain of a transmembrane protein and a polypeptide, where the compound that the protein with high throughput identification of compound that compound that phosphorylation-regulated cell signal transducers. (I) or efficiently detects multiple interaction between extracellular and compound that the sequence of antibiotic resistance enzyme TEM-1 beta-lactamase that can be used as a selectable gene in the fragment complementation system of the compound contraction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention describes a fragment complementation system (I) comprising a first oligopeptide having an N-terminal fragment with a C-terminal break-point, and a second oligopeptide having a C-terminal fragment with a N-terminal break-point, where the N-terminal fragment and the C-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fragment complementation system; marker protein; multiple genetic element incorporation; antibiotic resistance; beta-lactam derivative activation; anti-tumour compound; beta-lactam derivative activation; anti-tumour compound; functional reassembly; protein-protein interaction; proteome interaction; immunoglobulin variable region; immune cell protein; CD40; phosphorylation-regulated cell signal transducer; TEM-1 beta-lactamase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fragment complementation system for detecting immunoglobulin epitope, has first oligopeptide containing N-terminal fragment with C-terminal breakpoint, second oligopeptide containing C-terminal fragment with N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Balint RF,
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13-JAN-2000;
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99US-0135926P.
2000US-0175968P.
2000US-00526106.
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Seguence

263

Query Match
Best Local Similarity
Matches 149; Conserv

100.0%; ilarity 100.0%; Conservative (

0,

Score 770; DB 2; Pred. No. 7.9e-80; ; Mismatches 0;

Length 264;

0

Gaps

0

Sequence

264

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RESULT 4
ANALGG34
ID ANALGG34
ID ANALGG34
ID ANALGG34
ID O9-A
XX AAM1
AX Gene
KW Viru
KW Viru
KW HIV;
XX Esch
XX Esch
XX 29-y
FT Pept
FT Pept
FT Pept
XX 20-)
XX 29-y
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                                                                         Escherichia coli beta-lactamase (AAW16634), including the signal peptide, is the expression product of a molecular chimaera, designated pCMV-BL (AAT66737), in which the beta-lactamase gene is under control of the CMV intermediate/early promoter. Vectors consisting of a transcriptional regulatory DNA sequence linked to a beta-lactamase gene can be used for enzyme prodrug therapy. Expression of the beta-lactamase in a targetted cell allows conversion of a prodrug into an agent toxic to the cell for treatment of cancer, viral (e.g. HIV) infection or inflammation. Secretion of the enzyme has the advantage of increasing neighbouring cell
                                                                                                                                                                                                                                                                                                                                                    Example;
                                                                                                                                                                                                                                                                                                                                                                                                    Molecular chimaera for gene or virus directed enzyme useful for treatment of cancer, viral infection or in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             directed enzyme prodrug therapy; VDEPT; beta-lactamase; cancer;
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Pred. No. 7.8e-80;
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                                                                                                                                                                                                                                                                                                                                                                                                       nzyme prodrug therapy or inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            lactamase constructs, placed under control of promoter/enhancer elements of lung-associated protein or neuroendocrine marker protein genes, can be used in novel chimaeric molecules for use in prodrug therapy of lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The intracellular form (AAW18680) of TEM beta-lactamase is expressed pCMV-delBL (AAT70311) in which a PCR-amplified beta-lactamase coding sequence, minus the signal sequence, is placed under control of the intermediate/early promoter of cytomegalovirus. Intracellular beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA construct for gene-directed enzyme prodrug therapy of lung cancer comprises lung- or neuroendocrine-specific promoter controlling expression of prodrug-converting enzyme.
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                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 8iii; Page 32-34; 53pp; English.
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                                                                                                                                                                                                                                                                                                                                                          The expression constructs pRNH127 and pRNH155 contain identical sequences but were constructed using different strategies (see AAQ36498). The constructs comprise exons 2-7 of human CYP1A1 gene under the construct of the inducible mouse metallothionein (MMT-1) promoter. The constructs also contain an open reading frame in the opposite orientation to the cytochrome P450 exons. This ORF encodes ampicillin resistance. The constructs are suitable for transformation of human fibroblasts derived from the xeroderma pigmentosum group A. Cultures of the transformed fibroblasts can be used to test substances for mutagenicity. The presence of the inducible cytochrome P450 gene allows metabolism of the substance to mutagenic metabolites. (Updated on 10-MAR-2003 to add missing OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Col 21-24; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       In vitro method for testing mutagenicity of a chemical - by met chemical cell line consisting of transformed fibroblasts having detectable cytochrome P450 mixed function oxidase activity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5180666-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYP1A1; pRNH127; pRNH155; xeroderma pigmentosum group A; XPA; xenobiotics; circular; chimeric cytochrome P450IA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-MAR-2003
04-JUN-1993
                                                                                                                                                                                                                                                                                               Sequence 286 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    States JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYWA-) UNIV WAYNE STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JAN-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ampicillin resistance protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR31575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR31575 standard;
                                                                                                                                                                                                                       Local
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                                                                                                                                                                                              149;
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84
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                                                                                                                                                                                                                       Similarity
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                                                                                            HPETLYKYKDABDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KELTAFLHNMGDHVTRLDRWEPBLNEAIP 149
                                              AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KELTAFLHNMGDHVTRLDRWEPELNEAIP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hines RN,
                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
(first en
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91US-00721775.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
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                                                                                                                                                                                              <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RF;
                                                                                                                                                                                           Score 770; DB 2;
Pred. No. 8.8e-80;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
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121

KELTAFLHNMGDHVTRLDRWEPELNEAIP 149

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RESULT 8
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                                                                                                                                                                                                                                                                                                                                       the control of the intermediate/early cytomegalovirus promoter. Beta-lactamase delivery to mammalian cells confers sensitivity to cephalosporin prodrugs. Liposomal DNA/5-fluorouracil prodrug combinations resulted in s.c. tumour regression in mice bearing A549 tumours. Survival of mice bearing human large cell lung H460 intrathoracic (i.t.) tumours was increased upon i.t. injection of the secretory beta-lactamase DNA
                                                                                                                                                                                                                                                                                                                                                                                                                           A secretory beta-lactamase (AAR97619) is expressed from DNA construct pCMV-BL (AAT29220), in which the beta-lactamase coding sequence is under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecular chimaera for use in enzyme gene therapy - is activated in a target cell to express a secretable enzyme which cleaves a prodrug outside the cell into a cytotoxic or cytostatic agent.
 AAR96423 standard; protein; 286 AA.
                                                                                                                                                                                                                                                                                                 Sequence 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dev IK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09616179-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene therapy; gene directed enzyme prodrug therapy; GDEPT; virus directed enzyme prodrug therapy; VDEPT; prodrug activation; cytotextic; cancer; tumour; retrovirus; vector; beta-lactamase; cephalosporin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR97619 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Page 57-58; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-NOV-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Secretory beta-lactamase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-AUG-1996 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (WELL ) WELLCOME FOUND LTD.
                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1996-268615/27.
                                                                      144
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                                                                                                                                                                                                                                            149;
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                                                                                                                                             AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moore JT,
                                                                                     KELTAFLHNMGDHVTRLDRWEPELNEAIP 149
                                                                                                                                                                                                     HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                                                                                                                           AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 143
                                                                                                                                                                                    HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                                                                                                                                                                                                                                         100.0%;
llarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                       Score 770; DB 2;
Pred. No. 8.8e-80;
0; Mismatches 0;
                                                                      172
                                                                                                                                                                                                                                                                     Length 286;
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AAW16635 ID AAWI XX

AAW16635

standard; protein;

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RESULT 9

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Matches 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oxidase enyzmes expressed by the cells. Gene damage in the test cells is detected as an indication of cytotoxicity of the chemical. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Testing chemicals for cytotoxicity to human by using recombinant fibroblasts transformed with control of inducible promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytochrome; P450; metallothionein; mouse; metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is encoded by a chimeric mouse metallothionein-cytochrome P450IA1 (CYP1A1) expression construct. Two clones, pRNH12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Col 17-24; 26pp; English.
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09-DEC-1992;
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25-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                      HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                                             KELTAFLHNMGDHVTRLDRWEPELNEAIP 149
                                                                                                                                                                        AGQEQLGRRIHYSQNDLVEYSPVTEXHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                                                                                                                          AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                                                                                                                                                                                                                                                                HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
KELTAFLHNMGDHVTRLDRWEPELNEAIP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novak RF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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(first entry)
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92US-00990295.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 770; DB 2;
100.0%; Pred. No. 8.8e-80;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Best Local
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                                                                                                                                                                                                                                                                                                                                 Escherichia coli beta-lactamase (AAW16635), lacking the signal peptide, is the expression product of a molecular chimaera, designated pCMV-delBL (AAT66738), in which the beta-lactamase gene is under control of the CMV intermediate/early promoter. Vectors consisting of a transcriptional regulatory DNA sequence linked to a beta-lactamase gene can be used for enzyme prodrug therapy. Intracellular expression of the beta-lactamase in a targetted cell allows conversion of a prodrug into an agent toxic to the cell for treatment of cancer, viral (e.g. HIV) infection or
                                    Secretory beta-lactamase.
                                                        13-AUG-1997
                                                                                               AAW18679
                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecular chimaera for gene or virus directed enzyme prodrug therapy useful for treatment of cancer, viral infection or inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene directed enzyme prodrug therapy; ovirus directed enzyme prodrug therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-1997
      Prodrug therapy; gene directed enzyme prodrug therapy; GDEPT; virus directed enzyme prodrug therapy; VDEPT; lung cancer;
                                                                                                                                                                                                                                                                                                        Sequence 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                           Example; Page 26; 38pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-NOV-1995;
                                                                                                                                                                                                                                                                                                                            inflammation
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                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moore JT,
                                                                                               standard; protein;
                                                                                                                                                          KELTAFLHNMGDHVTRLDRWEPELNEAIP 149
                                                                                                                                                                                                  AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                                                                                                                                                       HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                                                                                                                                                                                    AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 143
                                                                                                                                                                                                                             HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                                                                                                                                               KELTAFLHNMGDHVTRLDRWEPELNEAIP 172
                                                                                                                                                                                                                                                                  Conservative
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                                                      (first entry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (no signal peptide).
                                                                                                                                                                                                                                                                          100.0%;
                                                                                               286
                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                 Score 770; DB 2;
Pred. No. 8.8e-80;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDEPT;
peta-lactamase; cancer;
                                                                                                                                                                                                                                                                                    Length 286;
                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                 0;
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       AAYO8529
ID AAYO8
XX AAYO8
AC AAYO8
XX AAYO8
DT O3-AU
DX Vecto
XX Firef
KW Firef
KW insec
KW aller
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Matches 149;
                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                              placed under control of the intermediate/early promoter of cytomegalovirus. Secretory beta-lactamase constructs, placed under control of promoter/enhancer elements of lung- associated protein or neuroendocrine marker protein genes, can be used in novel chimaeric molecules for use in prodrug therapy of lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                          The secreted form (AAW18679) of TBM beta-lactamase is expressed by pCMV-
BL (AAT70309) in which a PCR-amplified beta-lactamase coding sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA construct for gene-directed enzyme prodrug therapy of lung cancer -comprises lung- or neuroendocrine-specific promoter controlling expression of prodrug-converting enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Хeу
                                                                                                                                                                                                                                                                                                             Sequence 286 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 8ii; Page 26-27; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GLAX ) GLAXO GROUP LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          beta-lactamase; pCMV-BL.
                                                                                                                                                                                                                                               Local
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DB; AAT70309.
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                                                                                                                                                                                                                                               Similarity
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KELTAFLHNMGDHVTRLDRWEPELNEAIP 149
                                                                                                                                        HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                                                                                                                                                                HPETLYKYKDAEDQLGARVGYIBLDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60
                                                                                                AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sethna
                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           286
                                                         Score 770; DB 2; L
Pred. No. 8.8e-80;
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                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                     286;
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Firefly; luciferase; tetracycline; transcriptional control; TetR; tetracycline repressor; tetracycline promoter; luminescence; luxClinsect; Tn10; medicine; dosage; cheese production; antibiotic; foc

Vector pASK75 beta-la protein.

03-AUG-1999 AAY08529

(first

entry)

AAY08529 standard;

protein;

286

A

144

172

83

Synthetic

WO9925866-A1

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RESULT 12
AAB10442
ID AAB10
XX
AAB1040
XX
AC AAB10
DT 01-DE
XX
DE Expre
KW Expre
KW Expre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel tetracycline assay that uses recombinant CC prokaryotic cells comprising a luciferase gene under the transcriptional CC control of a tetracycline repressor and tetracycline promoter and CC involves the detection of luminescence emitted form the cells. The assay CC involves the detection of luminescence emitted form the cells. The assay CC can be used to distinguish tetracycline form other microbial agents. The CC invention also describes a novel plasmid comprising either the luxCDABB CC genes, a tetracycline repressor (TetR) and a tetracycline promoter (TetA) from Tn10. The tetracycline promoter (TetA) from Tn10. The tetracycline assay CC method can be used for the determination of tetracycline. The method can also be used for the determination of the medicine. The method can CC e.g. to study the dosage and penetration of the medicine. The method can also be used to test cheese production, as cheese making bacteria are not can be used to the presence of tetracycline. The method can also be used co determine the presence of tetracycline. The method can also be used concentration of antibiotics in foodstuffs, CC e.g. for allergic people. The present assay method does not rely on the growth of microbes as do conventional tests, and so is much more rapid. The present assay is also more sensitive, as even a small amount of luminescence can be detected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity Matches 149; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 286 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 47-48; 67pp; English:
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                                                                                                                                                              AAB10442 standard; protein; 286 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (KORP/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-NOV-1998;
                                                                                                                             AAB10442;
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                                                     Expression
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                                                                                                                                                                                                                                                           144
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) KARP M.
) KURITTU J.
                                                                                                                                                                                                                                                                                                                                                   AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                                                                                                                                                                                                                                                                                                                                         HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                                                                                                                                                                                                                                                                                KELTAFLHNMGDHVTRLDRWEPELNEAIP 149
                                                                                                                                                                                                                                                                                                                                AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 143
                                                                                                                                                                                                                                                                                                                                                                                                      HPETLVKVKDAEDQLGARVGYIBLDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for tetracycline using recombinant prokaryotic cells.
                                                                                                                                                                                                                                                           KELTAFLHNMGDHVTRLDRWEPELNEAIP 172
                                                     vector pSEX15G2 bla protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
ilarity 100.0%;
Conservative 0
                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 770; DB 2; Length 286;
Pred. No. 8.8e-80;
); Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Expression vector; antibody binding protein; monoclonal antibody; Neo-R; B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.

Expression vector; antibody binding protein; monoclonal antibody; Neo-R;

Expression vector pSEX11L4 bla protein

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RESULT 13
AAB10438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC This invention describes a novel method for the selection of monoclonal CC antibodies (MAb) which comprises (i) fusing B lymphocytes with myeloma CC cells to produce antibody-producing hybridomas such that the antibodies CC are presented at the surface of the hybridomas by an antibody-binding protein (I); and (ii) binding the antibody to antigens (Ag). The CC invention also describes antibody-binding proteins (I) that comprise a CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa CC thain or a murine MHC (major histocompatibility complex) Class I k(k) CC molecule; an antibody-binding site of proteins A, G, L or LG, and the CC transmembrane domain of PDGFR (platelet-derived growth factor receptor) CC or CD52. The method is used to select MAb with specificity for particular antigens. MAb can be selected without separate culture of hybridomas, and CC election can be made against many antigens in a library, optionally on CC mixtures of hybridomas can be used for selection, reducing the time and CC mixtures of hybridomas can be used for selection, reducing the time and CC cost involved in MAb selection. This sequence represents the bla protein CC bla protein, Neo-R and protein G described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 149
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                                                                  01-DEC-2000
                                                                                                                                 AAB10438 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Selecting monoclonal antibodies, by expressing them on the surface hybridomas attached to antibody-binding protein, then reaction with
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                          AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 143
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                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 286;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel method for the selection of monoclonal CC antibodies (MAb) which comprises (i) fusing B Jymphocytes with myeloma CC cells to produce antibody-producing hybridomas such that the antibodies CC are presented at the surface of the hybridomas by an antibody-binding protein (I); and (ii) binding the antibody to antigens (Ag). The CC invention also describes antibody-binding proteins (I) that comprise a CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa CC chain or a murine MHC (major histocompatibility complex) Class I k(k) CC molecule; an antibody-binding site of proteins A, G, L or LG, and the CC transmembrane domain of pogera (plattelet-derived growth factor receptor) CC or CD52. The method is used to select MAb with specificity for particular CC antigens. MAb can be selected without separate culture of hybridomas, and CC selection can be made against many antigens in a library, optionally on CC the basis of strength of affinity for a particular antigen. Complex CC mixtures of hybridomas can be used for selection, reducing the time and CC cost involved in MAb selection. This sequence represents the Neo-R CC cost involved in MAb selection. This sequence represents the Neo-R CC bla protein, Neo-R and protein G described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                 Expression vector pSEX11G2 bla protein
                                                                     01-DEC-2000
                                                                                                                                        AAB10440 standard; protein; 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 286 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Selecting monoclonal antibodies, by expressing them on the surface of hybridomas attached to antibody-binding protein, then reaction with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 16; Fig 1; 22pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                  . Local 149;
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                                                                                                                                                                                                                                   144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                               HPETLVKVKDAEDQLGARVGYIBLDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60
                                                                                                                                                                                                                                                        KELTAFLHNMGDHVTRLDRWEPELNEAIP 149
                                                                                                                                                                                                                                                                                                         AGQEQLGRRIHYSQNDLVEYSFVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGF 143
                                                                                                                                                                                                                                                                                                                             AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
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                                                                                                                                                                                                                                  KELTAFLHNMGDHVTRLDRWEPELNEAIP 172
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                                                                     (first entry)
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Pred. No. 8.8e-80;
); Mismatches 0;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein (I); and (ii) binding the antibody to antigens (Ag). The invention also describes antibody-binding proteins (I) that comprise a combination of the signal peptide of a murine immunoglobulin (Ig) kappa chain or a murine MHC (major histocompatibility complex) Class I k(k) molecule; an antibody-binding site of proteins A, G, L or LG, and the transmembrane domain of DGFR (platelet-derived growth factor receptor) or CD52. The method is used to select MAb with specificity for particular antigens. MAb can be selected without separate culture of hybridomas, and selection can be made against many antigens in a library, optionally on the basis of strength of affinity for a particular antigen. Complex mixtures of hybridomas can be used for selection, reducing the time and cost involved in MAb selection. This sequence represents the bla protein protein contained in the expression vector pSEXIIG2 which contains the bla protein, Neo-R and protein G described in the method of the invention
                                                                                                         AAB50898 standard; protein; 286 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 286 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cells to produce antibody-producing hybridomas such that the antibodies are presented at the surface of the hybridomas by an antibody-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel method for the selection of monoclonal antibodies (MAb) which comprises (i) fusing B lymphocytes with myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hybridomas attached to antibody library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Breitling F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Expression vector; antibody binding protein; monoclonal antibody; Neo-R; B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Selecting monoclonal
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                                                                                                                                                                                                                                                                                              AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                                                                                                                                                                                                                                                                 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 83
                                                                                                                                                                                                                                                                                                                                                                    HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60
                                                                                                                                                                                                  KELTAFLHNMGDHVTRLDRWEPELNEAIP 172
                                                                                                                                                                                                                                                                            AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fig 2; 22pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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Pred. No. 8.8e-80;
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Protein encoded by bla resistance marker of integration vector pLO12306

20-MAR-2001 AAB50898;

(first entry)

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                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant host cells useful for producing polysaccharase for degrading oligosaccharides, comprises a first heterologous polynucleotide encoding polysaccharase under control of surrogate promoter.
                                                                                                                                                                                                                                                                                                                                        Sequence 286 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bla resistance marker; recombinant host cell; saccharification; fermentation; polysaccharase; oligosaccharide degradation; celZ gene; glucanase; integration vector; pLO12306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-032043/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ingram LO,
                                                                                                                                                                                                                                                                                                                                                                                                     chrysanthemi, resistance markers bla and tet, and Klebsiella oxytoca
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                                                                                                                                                                                                                                                    y Match 100.0%; Score 770; DB 4; Length 286; Local Similarity 100.0%; Pred. No. 8.8e-80; hes 149; Conservative 0; Mismatches 0; Indels
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                   KELTAFLHNMGDHVTRLDRWEPELNEAIP 149
                                                                                                              AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                   AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 143
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KELTAFLHNMGDHVTRLDRWEPELNEAIP 172
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Search completed: June 10, 2005, 10:49:11 Job time : 58.7711 secs

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Q00626 staphylococ
Q79c16 methylobaci
Q79dr3 escherichia
P62593 escherichia
P62594 salmonella
Q6a253 haemophilus
Q6lbn9 pseudomonas
Q6lcv6 neisseria g
Q6tmh1 streptococc
Q6w9j1 enterobacte
Q6wr22 zymomonas m
Q6wz44 acinetobacte
Q7b3x5 citrobacter
Q7b3x5 citrobacter
Q7b3x5 citrobacter
Q7b3x5 citrobacter
Q7b3x5 shigella fl
Q7br75 neisseria m
Q7dfy3 salmonella
Q7dfy3 salmonella
Q7dhy3 plasmid pet
Q8ksd2 escherichia
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63	ADK:	BAIPND	PVTEKHLTDGMTVRE	IELDLNSGKILES	No.	e. e_A. e_A. 2P2275:	DOI=10	ae; Mic	ed) sequenci annotat	286	ALIGNMENTS		
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C Q00628; 008029; 0080102; 009403; 009404; 009405; 009406
C 009408; 009481; 009482; 009483; 009490; Q57339;
T 01-NOV-1996 (TrEMBLrel 01, Created)
T 25-OCT-2004 (TrEMBLrel 28, Last annotation update)
E 8eta-lactamase.
S $taphylococcus aureus.
S $taphylococcus aureus; Bacillales; $taphylococcus.
C Bacteria; Firmicutes; Bacillales; $taphylococcus.
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Q79CL6;
05-JUL-2004
   SEQUENCE FROM N.A.
MEDLINE=97074643;
Serebrijski I.G.,
                                                                                               Methylobacillus flagellatum.
Bacteria; Proteobacteria; Betaproteobacteria; Methylophilales;
Methylophilaceae; Methylobacillus.
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
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MEDLINE=96422755; PubMed=8825372; DOI=10.1006/plas.1995.0005;
Needham C., Noble W. C., Dyke K. G.;
"The staphylococcal insertion sequence IS257 is active.";
Plasmid 34:198-205(1995).
EMBL; U36912; AAB39957.1; -.
EMBL; U36911; AAB39956.1; -.
                                                                           NCBI_TaxID=405;
                                                                                                                                                       Name=bla;
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   PubMed=8917070; DOI=10.1016/0378-1119(96)00114-X; Vassin V.M., Tsygankov Y.D.;
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Q79DR3;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Mutant extended-spectrum beta-lactamase precursor (Name=bla; Synonyms=blaTEM-116;
Escherichia_coli
                                                                                                                                    Rondot S.,
Little M.,
   MEDLINE=98189310; PubMed=9514792; DOI=10.1006/abio.1997.2558; Schlieper D., Von Wilcken-Bergmann B., Schmidt M., Sobek H., Mueller-Hill B.;
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Submitted (UUL-1995) to the EMBL/GenBar
EMBL; U31280; AAC44581.1; -.
HSSP; P00807; 1ALQ.
Interpro; IPR001466; Beta_lactamase.
Interpro; IPR0018971; Beta_lactamase A.
Pfam; PF00144; Beta_lactamase; 1.
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                                                          SEQUENCE PROM N.A. PLASMID=PCAPs;
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STRAIN=K12; PLASMID=pRP4;
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STRAIN=K-12;
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Bacteria; Proteobacteria; Gammaproteobacteria;
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BLAT ECOLI STANDARD; PRT; 286 AA.

P62593; P00810; Q47313;

21-JUL-1986 (Rel. 01, Created)

21-JUL-1986 (Rel. 01, Last sequence update)

25-JAN-2005 (Rel. 46, Last amootation update)

Beta-lactamase TEM precursor (BC 3.5.2.6) (TEM-1) (TEM-2)

(TEM-4) (TEM-5) (TEM-6) (TEM-8/CAZ-2) (TEM-16/CAZ-7) (TEM-
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J. Clin. Microbiol. 42:290-2906(2004).
EMBL; M74750; AAA24057.1; -.
EMBL; Y12694; CAA73286.1; -.
EMBL; AJ001614; CAA73286.1; -.
EMBL; AY425988; AAQ95605.1; -.
EMBL; AY425988; AAQ95605.1; -.
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Jeong S.H., Bae I.K., Lee J.H., Sohn Kim Y.H., Jeong B.C., Lee S.H., Sohn Kim Y.H., Jeong B.C., Lee S.H., Sohn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE_A;
                            Name=blaT-5;
                                                    Name=blaT-4;
                                                                               Name=blaT-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase; Plasmid; Signal.
SIGNAL 1 23
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    Name=blaT-6;
                                                                                                                    (IRT-4) (Penicillinase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A positive selection vector for cloning of reaction fragments based on a lethal mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular Characterization of Extended-Spectrum Beta-Lactamases
                                                                                                                                                                                                                                                                            264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fragments
hia coli."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HPETLVKVKDAEDQLGARVGY1ELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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Pred. No. 2.1e-96;
; Mismatches 0;
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                                                                                                                                 (TEM-24/CAZ-6)
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                                                                                                                                             (TEM-3)
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[5]
SEQUENCE .
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Plasmid R1 (R7268), Plasmid IncFII R100, Plasmiu Av., --
Plasmid pCFF04, and Plasmid pCFF14.

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

Proteophacteriaceae; Escherichia.
                                    MEDLINE=92166702; PubMed=1665171;
Goussard S., Sougakoff W., Mabilat C., Bauernfeind A., Courv.
"An IS1-11ke element is responsible for high-level synthesis
extended-spectrum beta-lactamase TEM-6 in Enterobacteriaceae
J. Gen. Microbiol. 137:2681-2687(1991).
                                                                                             STRAIN=CB86134; PLASMID=pCFF04, and pUD16;
MEDLINE=89378760; PubMed=2550326; DOI=10.1016/0378-1119(89)90236-9;
Sougakoff W., Petit A., Goussard S., Sirot D., Bure A., Courvalin P
"Characterization of the plasmid genes blaT-4 and blaT-5 which enco-
the broad-spectrum beta-lactamases TEM-4 and TEM-5 in
enterobacteriaceae.";
                                                                                                                                                                                                                                                                  Mabilat C., Lourencao-Vital J., Goussard S., Courvalin P.; 
"A new example of physical linkage between Th1 and Th21: the 
antibiotic multiple-resistance region of plasmid pCFF04 encoding 
extended-spectrum beta-lactamase TEM-3."; 
mol. Gen. Genet. 235:113-121(1992).
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Sutcliffe J.G.;
SEQUENCE FROM N.A. MEDLINE=93037315;
                                                                                                                                                                                                                                                                                                                                                                                                   Sougakoff W., Goussard S., Courvalin P.;
"The TEM-3 beta-lactamase, which hydrolyzo
cephalosporins, is derived from the TEM-2
acid substitutions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=86319522; PubMed=3019092; I
Ohtsubo H., Ryder T.B., Maeda Y., /
"DNA replication of the resistance
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                                                                                                                                               Gene
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                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (TEM-3).
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MEDLINE=93062798; PubMed=1331747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLASMID=R6K; TRANSPOSON=Tn1;
MEDLINE=79012483; PubMed=358199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 24-286
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PLASMID=IncFII R100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete nucleotide sequence pBR322.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Partial amino acid sequence of penicillinase coded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ambler R.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Nucleotide sequence of the ampicillin coli plasmid pBR322.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plasmid R6K."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biophys. 21:115-133(1986).
                                                                                                                                               78:339-348(1989).
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); TRANSPOSON=Tn3;
PubMed=358200;
PubMed=1416873;
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which hydrolyzes broad-spectrum
the TEM-2 penicillinase by
           TEM-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the
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             AND
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Armstrong K., Ohtsubo E.;
e plasmid R100 and its control.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli plasmid
             TEM-24)
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                                                                            Courvalin
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Mobashery S., Samama J.-P.;
"X-ray structure of the Asn276Asp variant of the Escherichia coli TEM-
"Beta-lactamase: direct observation of electrostatic modulation in resistance to inactivation by clavulanic acid.";
Biochemistry 38:9570-9576(1999).
-i- FUNCTION: TEM-type are the most prevalent beta-lactamases in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96186252; PubMed=8605632; Strynadka N.C.J., Jensen S.E., Alzari P.M., James M.N.G.; Strynadka n.C.J., Jensen S.E., Alzari P.M., James M.N.G.; "A potent new mode of beta-lactamase inhibition revealed by X-ray crystallographic structure of the TEM-1-BLIP complex. Nat. Struct. Biol. 3:290-297(1996).
                                        the
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MEDLLNB=98153145; PubMed=9485412; DOI=10.1021/bi972501b;
Maveyraud L., Pratt R.F., Samama J.-P.;
"Crystal structure of an acylation transition-state analog of the TEM-
1 beta-lactamase. Mechanistic implications for class A beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93361453; PubMed=8356032;
Jelsch C., Mourey L., Masson J.-M., Samama J.-P.;
"Crystal structure of Escherichia coli TEM1 beta-lactamase
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MEDLINE=92183921; PubMed=1544485; DOI=10.1016/0014-5793(92)80232-6;
Jelsch C., Lenfant F., Masson J.-M., Samama J.-P.;
"Beta-lactamase TEM1 of E. coli. Crystal structure determination at 2.5-A resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Characterization and amino acid sequence of IRT-4, a novel TEM-type enzyme with a decreased susceptibility to beta-lactamase inhibitors."; FEMS Microbiol. Lett. 120:111-117(1994).
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MEDLINE=99352177; PubMed=10423234; DOI=10.1021/bi990758z;
Swaren P., Golemi D., Cabantous S., Bulychev A., Maveyraud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS)
MEDLINE=96186252; PubMed=8605632;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chanal C., I
                                                                                                                    between
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                                    ween the Swiss Institute of Bioinforma
European Bioinformatics Institute. The
by non-profit institutions as long
                                                                                                                                                                                                                                                                                                          amino acid.

BIOTECHNOLOGY: This protein is used as a marker in many commonly used cloning vectors, such as pBR322 and the pUC series.

MISCELLANEOUS: The beta-lactamase present on pBR322 was cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enterobacteria; they hydrolyze the beta-lactam bond in susceptible beta-lactam antibiotics, thus conferring resistance to penicillins and cephalosporins. TEM-3 and TEM-4 are capable of hydrolyzing cefotaxime and ceftazidime. TEM-5 is capable of hydrolyzing ceftazidime. TEM-6 is capable of hydrolyzing ceftazidime. TEM-6 is capable of hydrolyzing ceftazidime. TEM-8/CAZ-2, TEM-16/CAZ-7 and TEM-24/CAZ-6 are markedly aztreonam. TEM-8/CAZ-2, TEM-16/CAZ-7 and TEM-24/CAZ-6 are markedly
                                                                                                                                                                                                                             from plasmid R1 (R7268). SIMILARITY: Belongs to the class-A beta-lactamase family.
                                    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: A beta-lactam + H(2)0 = a substituted beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           active against ceftazidime. IRT-4 shows resistance lactamase inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lett. 299:135-142(1992).
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statement is not removed.
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EMBL; V00613; CAA23886.1;
EMBL; X64523; CAA45828.1;
EMBL; X57972; CAA41038.1;
EMBL; X65252; CAA46344.1;
EMBL; X65252; CAA46344.1;
EMBL; X65253; CAA46346.1;
EMBL; X65254; CAA46346.1;
EMBL; U89928; AAB64386.1;
EMBL; U66885; AAC48875.1;
      SALTI
BLAT SALTI STANDARD; PRT; 286 AA.

P62594; P00810; Q47313;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Beta-lactamase TEM precursor (EC 3.5.2.6) (Penicillinase).
Name=bla; OrderedLocusNames=HCM1.216;
Salmonella typhi.
                                                                                                                                                                                                                                                                                                                      PDB;
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1BT5; X:
1BTL; X:
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1ERM; X:
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1FQG;
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                                                                                                                SQATMDERNROIAEIGASLIKHW
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                                                                                                                                          QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG
                                                                                                                                                                       KELTAPLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ
                                                                                                                                                                                               AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                                                                                                               AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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    Mismatches

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Pred. No. 5.1e-96;
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Best Local S
Matches 261
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                      DISULFID SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 413:848-852(2001).

-i- FUNCTION: TEM-type are the most prevalent beta-lactamases in enterobacteria; they hydrolyze the beta-lactam bond in susceptible beta-lactam antibiotics, thus conferring resistance to penicillins and cephalosporins (By similarity).

-i- CATALYTIC ACTIVITY: A beta-lactam + H(2)0 = a substituted beta-
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Antibiotic
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STRAIN=CT18;
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NCBI_TaxID=601;
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InterPro; IPR000871; Beta_lactamase_A.
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                         241
                                                             204
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PRO0118; BLEACTAWASEA.

2; PS00146; BETA_LACTAWASE_A; 1.

2; PS00146; BETA_LACTAWASE_A; 1.

By similarity.

By similarity.

Pro-lactamase TEM.
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                                                             QLIDWMEADKVAGFLLRSALFAGWFIADKSGAGERGSRGIIAALGFDGKFSRIVVIYTTG
SQATMDERNRQIAEIGASLIKHW
                      SQATMDERNRQIAEIGASLIKHW
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                                                                                                                                                                                                                                                                                                                      Score 1343; DB 1;
Pred. No. 5.1e-96;
1; Mismatches 1;
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Acyl-ester intermediate (By similarity)
Proton acceptor (By similarity).
Substrate binding (By similarity).
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                            263
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Q6LEN9 PRELIMINARY;
Q6LEN9;
Q5-JUL-2004 (TrEMBLrel. 27, C
Q5-JUL-2004 (TrEMBLrel. 27, L
Q5-CCT-2004 (TrEMBLrel. 28, L
Penicillinase TEM-1.
Name=bla(tem-1A); Synonyms=bl
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EMBL; AJ627386; CAF29065.1; -.
GO: GO:00008800; F:beta-lactamase activity;
GO: GO:0016787; F:hydrolase activity; IEA.
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PROSITE; PS00146; BETA_LACTAMASE_A;
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"Molecular biology
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1. 28, Last sequence update,
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SEQUENCE
           MEDLINE=20079289; PubMed=10610817; DOI=10.1006/plas.1999.1431; Pagotto F., Aman A.T., Ng L.K., Yeung K.H., Brett M., Dillon J "Sequence analysis of the family of penicillinase-producing ploof Neisseria gonorrhoeae.";
                                                                                                                                                                                                                                                                                                                               MEDLINE=99225589; PubMed=10208798; DOI=10.1006/mcpr.1998.0216; Dillon J.R., Li H., Yeung K.-H., Aman T.A.; "A PCR assay for discriminating Neisseria gonorrhoeaebeta-lact
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Neisseriaceae; Neisseria.
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InterPro; IPR000871; Beta_lactamase_A.
Pfam; PF001144; Beta_lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
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"Sequence of the genes blaT-1B and blaT-2.";
Gene 102:71-73[1991].
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MEDLINE=91323733; PubMed=1650734; DOI=10.1016/0378-1119(91)90540-R;
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Bacteria; Proteobacteria; Gammaproteobacteria;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                 producing Mol. Cell.
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                                                                                                                                                                                           SEQUENCE FROM N.A.
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Pred. No. 5.1e-96;
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PROSITE;
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Submitted (SEP-2003) to the
EMBL; AY392531; AAQ94057.1;
HSSP; P00807; 1ALQ.
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HSSP; P00807; 1ALQ.
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; PSO0146; BETA LACTAMASE A; 1.
E 286 AA; 31515 MW; BB678943BB18934B
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Q6W9J1;
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05-JUL-2004 (TrEMBLrel. 2:
05-JUL-2004 (TrEMBLrel. 2:
TEM-1 beta-lactamase.
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Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases
EMBL; AY302260; AAQ73497.1; -.
HSSP; PO0807; 1ALQ.
InterPro; IPR001466; Beta lactamase.
InterPro; IPR001871; Beta_lactamase_A.
Pfam; PF00114; Beta_lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA LACTAMASE A; 1.
EROSITE; PS00146; BETA LACTAMASE A; 1.
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Bacteria; Proteobacteria; Gammapr
Enterobacteriaceae; Enterobacter.
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27,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1343; DB
Pred. No. 5.1e-9
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ databases.
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Last annotation updat
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DT Q5-U0
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OX NCB1_
RP SEQUI
RC STRAI
RA Submi.
RN [2]
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Matches 261;
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Q6WRX2;
Q6WRX2;
05-JUL-2004 (TrEMBLrel. 2:
05-JUL-2004 (TrEMBLrel. 2:
05-JUL-2004 (TrEMBLrel. 2:
Beta-lactamase TEM-1.
                                                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 2
05-JUL-2004 (TrEMBLrel. 2
25-OCT-2004 (TrEMBLrel. 2
Beta-lactamase TEM-1.
Name=blaTEM-1;
Huang Z.,
Submitted
[2]
                                                                                                                                                                                                                                                                                                                                                                                              Q6WZD4;
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Cagno J., Katz S.E.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY271877; AAQ02307.1; -.
HSSP; P00807; 1ALQ.
InterPro; IPR001466; Beta_lactamase.
InterPro; IPR000971; Beta_lactamase_A.
Pfam; PF00144; Beta_lactamase; 1.
PRINTS; PR00118; BELACTAMASEA,
PROSITE; PS00146; BETA_LACTAMASE A; 1.
EXQUENCE 286 AA; 31515 MW; BB678943BB18934B CRC64;
                                                                                                                                                      Bacteria; Proteobacteria; Gar
Moraxellaceae; Acinetobacter
MCBI_TaxID=470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zymomonas mobilis.
Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadaceae; Zymomonas.
                                                                         STRAIN-HZ40;
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                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                        Acinetobacter baumannii.
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                              Chen Y., Mao 1
(MAR-2003) to
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99.2%; Pred. No. 5.1e-96;
tive 1; Mismatches 1;
                              P., Wu J., Wu L., Shan the EMBL/GenBank/DDBJ
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InterPro; IPR001466; Beta_lactamase.
InterPro; IPR001471; Beta_lactamase.
Pfam; PF00144; Beta_lactamase; 1.
                                                                                                                                                                                                                                               Ceglowski P.;
Submitted (OCT-2002) to the EMBL/GenBa:
EMBL; AF550415; AAN87698.1; -
HSSP; P00807; IALQ.
InterPro; IPR001466; Beta_lactamase.
InterPro; IPR001871; Beta_lactamase.
InterPro; IPR001871; Beta_lactamase.
InterPro; IPR001871; Beta_lactamase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=blaTEM1;
Citrobacter freundii.
Plasmid pCTX-M3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00118; BLACTAMASEA.

PROSITE; PS00146; BETA LACTAMASE A; 1.

SEQUENCE 286 AA; 31515 MW; BB678943BB18934B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   Golebiewski
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria;
                                                                                                                                                                                  Plasmid.
                                                                                                                                                                                                                                PRINTS; PRO0118; BLACTAMASEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BlaTEM1.
                                                                                                                                                                                                      PROSITE; PS00146; BETA_LACTAMASE_A; 1.
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thes 261;
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                                                                                                                                                             286 AA;
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                                                                                                                                                          31515 MW;
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                                                            ; Score 1343; DI
; Pred. No. 5.1e.
1; Mismatches
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EMBL/GenBank/DDBJ databases.
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Last annotation update)
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Pred. No. 5.1e-96;
1; Mismatches 1;
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Q7B899;
05-JUL-2004
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Submitted
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25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
TEM beta-lactamase (BlaTEM-1b beta-lactamase) (Beta
                   SEQUENCE FROM N.A.

PubMed=14613957;

Nelson E.C., Segal H., Elisha B.G.;

"Outer membrane protein alterations and blaTEM-1 variants:
in beta-lactam resistance in Klebsiella pneumoniae.";
J. Antimicrob. Chemother. 52:899-903(2003).
                                                                                                                                                                                                          STRAIN=kpn99-1029; PLASMID=pkpn99-1029; Xiong Z., Zhu D., Wang F., Zhang Y.; "Study on the encoding gene of extended-spectrum Klebsiella pneumoniae isolate.";
                                                                                                                                                                                                                                                                                                                                                                              Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLASMID=pJHCMW1;
MBDLINE=22270945; PubMed=12384346;
MSDLINE=22270945; PubMed=12384346;
Sarno R., McGillivary G., Sherratt D.J., Actis L.A.,
"Complete nucleotide sequence of Klebsiella pneumonia plasmid pJHCMW1.";
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Klebsiella pneumoniae.
Plasmid pHMCMW1, Plasmid pRMH760, Plasm
Bacteria; Proteobacteria; Gammaproteoba
  EMBL; AF479774;
                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                       PLASMID=E3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
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Tolmasky M.E.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterobacteriaceae; Klebsiella.
                                                                                                                                                                                         Zhongguo Kang Sheng
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLASMID=pRMH760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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1 (JAN-2004)
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                                                                                                                                                                                                                                                                                                                                                        Zhou W., Yu Y.;
(SEP-2000) to
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to the EMBL/GenBank/DDBJ
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EMBL; AF309824; AAG47772.1; -.
EMBL; AY293072; AAP43782.1; -.
EMBL; AY394610; AAQ96920.1; -.
HSSP; P00807; 1ALQ.
InterPro; IPR001466; Beta_lactamase.
InterPro; IPR001971; Beta_lactamase_A.
Pfam; PF00144; Beta_lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASEA.
Plasmid.
SEQUENCE 286 AA; 31515 MW; BB678943BI
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beta-lactamase (EC bla protein - Pseu beta-lactamase (EC probable Beta lact beta-lactamase (EC
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Yeast 13, 1065-1075, 1997
A;Title: Heterologous HIS3 marker and GPP reporter modules for PCR-target A;Reference number: Z09587
A;Accession: T51301
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T51301
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C;Superfamily: beta-lactamase
C;Keywords: hydrolase
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C;Species: Schizosaccharomyces pombe
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C;Accession: T51301
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from GB/EMBL/DDBJ

GFP reporter modules for PCR-targeting

in

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Result No.

Minimum

Maximum

Database

37.4 37.4 37.4 36.5	45	44	43	42	41	40	9	38	37	36	<u>3</u> 5	ω 4	u u	32	31	5
263 2 AS4433 291 2 S42075 302 2 S36188 294 2 S16553 306 1 B45822 306 2 G47330 291 2 JP0074 305 2 A61156 305 2 A61156 305 2 A6080 314 2 S06967 294 2 S19006 314 2 S19006 305 2 S19006	464.5	468.5	472	478	480.5	480.5	480.5	482	488.5	489.5	492.5	492.5	493.5	502.5	503.5	509
2 A54543 2 A54543 2 S42075 2 S365188 2 S16553 1 B45822 2 G69674 2 S47330 2 JP0074 2 A61156 2 A61156 2 A61600 2 A60600 2 S06967 2 S06967 2 S06967 2 S06967 2 S06967	34.5	34.8	35.0	35.5	35.6	35.6	35.6	35.8	36.2	36.3	36.5	36.5	36.6	37.3	37.4	٤/. ٥
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beta-lactamase	S03167	S19006	823929	S06967	A60680	A57002	A61156	JP0074	S47330	G69674	B45822	S16553	S36188	S42075	A54543	04070R

ALIGNMENTS

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RESULT 2
847061
beta-lactamase (EC 3.5.2.6) - phage phi-X174
C:Species: phage phi-X174
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S47061
C:Accession: S47061
R; Henrich, B.; Schmidtberger, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263; Conservative
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beta-lactamase (EC 3.5.2.6) precursor - synthetic C;Species: synthetic C;Species: synthetic C;Date: 25-Dec-1994 #sequence_revision 22-Aug-1996 #text_change 20-C;Accession: $41975 R;Kaestner, K.H.; Montoliu, L.; Kern, H.; Thulke, M.; Schutz, G. Gene 148, 67-70, 1994 A;Title: Universal beta-galactosidase cloning vectors for promoter A;Reference number: A57991; MUID:95011660; PMID:7926839 A;Accession: $41975 A;Accession: $41975 A;Status: not compared with conceptual translation
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A;Cross-references: UNITROT:038058;
C;Superfamily: beta-lactamase I
C;Keywords: hydrolase
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A;Description: A variant of phiX174 gene B-based positive selection vectors with enhance
A;Reference number: S47060
A;Accession: S47061
A;Status: preliminary
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A; Residues: 1-286 < KAE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Date: 25-Dec-1994 #sequence_revision 22-Aug-1996 #text_change 20-Oct-2000
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                      QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG
                                                                                                KELTAFIHNMGDHVTRLDRWEPELNEAIFNDERDTTMPVAMATTLRKLLTGELLTLASRQ
                                                                                                                                                                            AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                                                                                                                                HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                                                                                                                                                                                                                                                HPETLYKYKDAEDQLGARVGYIELDLNSGKILESFRPEBRFPMMSTFKVLLCGAVLSRID
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                                                                          KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ
                                                                                                                                                      AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG
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                                                                                                                                                                                                                                                                                                         Score 1348; DB 4;
Pred. No. 1.2e-105;
Mismatches 0;
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Pred. No. 1.2e-105;
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A;Residues: 182-286 <KOR>
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                                                                                                                                    Local Similarity
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                                      24 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRVD
AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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beta-lactamase (EC 3.5.2.6) precursor - Escherichia coli plasmids N;Alternate names: beta-lactamase TEM-6 (for blaT-6 DNA); penicillinase C;Species: Escherichia coli C;Date: 30-Nov-1980 #sequence revision 01-Sep-1981 #text_change 16-Aug-2004 C;Accession: A93821; A93820; A35387; S24415; A01005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross references: UNIPROT: D00810; GB: V00613; GB: J01832; NI A;Experimental source: plasmid pBR322 R;Ambler; R.D.; Scott, G.K. Proc. Natl. Acad. Sci. U.S.A. 75, 3732-3736, 1978 A;Title: Partial amino acid sequence of penicillinase coded A;Reference number: A93820; MUID: 79012483; PMID: 358199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rroc. Natl. Acad. Sci. U.S.A. 75, 3737-3741, 1978
A;Title: Nucleotide sequence of the ampicillin resistance A;Reference number: A93821; MUID:79012484; PMID:358200
A;Accession: A93821
A:Moleonic A93821
                                                                                                                                                                                                                                                 C;Keywords: antibiotic resistance; hydrolase; membrane protein F;1-23Domain: signal sequence #status predicted <SIG>F;24-286/Product: beta-lactamase #status experimental <MAT>F;68/Active site: Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cold Spring Harb. Symp. Quant. Biol. 43, 77-90, 1979 A;Title: Complete nucleotide sequence of the Escherichia A;Reference number: A90923; MUID:80002802; PMID:383387 A;Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-101,'K',103-161,'H',163-286 <GOU>
A;Cross-references: EMBL:X57972; NID:g41816; PIDN:CAA41038.1; PID:g41817
A;Experimental source: ISI-like blaT-6 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Goussard, S.; Sougakoff, W.; Mabilat, C.; Bauernfeind, A.; Courvalin, P.
J. Gen. Microbiol. 137, 2681-2687, 1991
A;Title: An IS1-like element is responsible for high-level synthesis of extended-spectrum A;Reference number: S24415, MUID:92166702; PMID:1665171
A;Accession: S24415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Experimental source: plasmid R6K
R;Kornacki, J.A.; Burlage, R.S.; Figurski, D.H.
J. Bacteriol. 172, 3040-3050, 1990
A;Title: The kil-kor regulon of broad-host-range plasmid
A;Reference number: A35387; MUID:90264294; PMID:2160936
A;Accession: A35387
                                                                                                                                                                                                                                                                                                                                                                                         A;Genome: plasmid
C;Superfamily: Beta-lactamase I
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A;Residues: 24-36,'K',38-286 <AMB>
1 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60
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                                                                                       Conservative
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                                                                                   Score 1343; DB 1;
Pred. No. 3.1e-105;
1; Mismatches 1;
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extended spectrum beta-lactamase CAZ-7 - Klebsiella pneumoniae C;Species: Klebsiella pneumoniae C;Species: Klebsiella pneumoniae C;Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 22-Jun-1999 C;Accession: $60312 R;Chanal, C.; Poupart, M.C.; Sirot, D.; Labia, R.; Sirot, J.; Cluzel, R. Antimicrob. Agents Chemother. 36, 1817-1820, 1992 A;Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes. A;Reference number: $60310; MUID:93037315; PMID:1416873 A;Recession: $60312 A;Status: preliminary; translation not shown A;Molecule type: DNA A;Residues: 1-286 <CHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Note: cloning vector pCG1408 engineered and expressed in Clavibacter xyli (;Date: 15-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Oct-2000 C;Accession: I40905 R;Taylor, J; Stearman, R.S.; Uratani, B.B. Plasmid 29, 241-244, 1993 A;Title: Development of a native plasmid as a cloning vector in Clavibacter: A;Reference number: I40904; MUID:93361581; pMID:7689234 A;Accession: I40905 A;Accession: I40905 A;Status: preliminary; translated from GB/EMBI/DDBJ
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A; Residues: 1-286 < RES>
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C;Superfamily: beta-lactamase I
C;Keywords: antibiotic resistance; hydrolase
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Matches 258
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Local Similarity 98.1%;
les 258; Conservative
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nes 258; Conserv
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98.1%;
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Pred. No. 4.6e-104;
3; Mismatches 2;
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Pred. No. 3.8e-104;
3; Mismatches 2;
                                                 263
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A;Cross-references: EMBL:X65254; NID:g296955; PIDN:CAA46346.1; PID:g296956 C;Superfamily: beta-lactamase I
QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG
                                          QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG
                                                                                                                                               KELTAFLHNMGDHVTRLDRWEFELNEAIPNDERDTTMFVAMATTLRKLLTGELLTLASRQ 180
                                                                                                                                                                                                                               AGQEQLGRRIHYSQNDLVKYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                                                                                                                                                        AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                                                                                                                                                                                                                                                        HPETLVKVKDAEDKLGARVGYIBLDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRVD
                                                                                                                                                                                                                                                                                                                                                                        HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                                                                                                                     KELTAFLHNMGDHVTRLDHWEPELNEAIPNDERDTTMPAAMATTLRKLLTGELLTLASRQ
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R;Mabilat, C.; Lourencao-Vital, J.; Goussard, S.; Courvalin, Mol. Gen. Genet. 235, 113-121, 1992
A;Title: A new example of physical linkage between Tn1 and TA;Reference number: S30112; MUID:93062798; PMID:1331747
A;Accession: S30113 beta-lactamase (EC 3.5.2.6) TEM-3 - Klebsiella pneumoniae plasmid pCFF04 C;Species: Klebsiella pneumoniae C;Species: Klebsiella pneumoniae C;Date: 30-Sep_1993 #sequence_revision 30-Sep_1993 #text_change 09-Jul-2:C;Accession: S30113 A;Cross-references: UNIPROT:P00810; EMBL:X64523; NID:g43797; PIDN:CAA45828.1; PID:g43798 between Tn1 and Tn21: PMID:1331747 the antibiotic multiple

Length 286; Indels 0 Gaps 0

HPETLYKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG KELTAFLHNMGDHVTRLDRWEFELNEAIPNDERDTTMFVAMATTLRKLLTGELLTLASRQ 180 AGQEQLGRRIHYSQNDLVKYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120 KELTAFLHNMGDHVTRLDRWEPELNEAI PNDERDTTMPAAMATTLRKLLTGELLTLASRQ 240 143 83 60 263 203

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A;Molecule type: DNA
A;Residues: 1-32 <TOL>
A;Cross - references: GB:M55547; N:
C;Genetics:
C;Genetics: DIA
A;Gene: TEM-bla
C;Superfamily: beta-lactamase I
C;Keywords: antibiotic resistance
                                                                                                                                                                                                                                                                                                                                                              beta-lactamase (EC 3.5.2.6) TEM-1 - Klebsiella pneumoniae transposon Tn131 C;Species: Klebsiella pneumoniae
C;Date: 12-Apr-1996 #sequence revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: S60311; F37392; PQ0498
R;Chanal, C.; Poupart, M.C.; Sirot, D.; Labia, R.; Sirot, J.; Cluzel, R.
Antimicrob. Agents Chemother. 36, 1817-1820, 1992
A;Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.
A;Reference number: S60310; MUID:93037315; PMID:1416873
A;Accession: S60311
A;Scatus: preliminary; translation not shown
A;Residues: 1-286 <CHA>
A;Cross-references: UNIPROT:Q99224; EMBL:X65253; NID:g296953; PIDN:CAA46345.1;
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                                                                                                                                                                                                                                            R;Tolmasky, M.E. Plasmid 24, 218-226, 1990 Plasmid 24, 218-226, 1990 A;Title: Sequencing and expression of aadA, bla, and tnpR A;Reference number: A37392; MUID:91172904; PMID:1963948 A;Accession: F37392
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                                                                                                Gene: TEM-bla
Superfamily: beta-lactamase I
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97.3%;
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Pred. No. 1.5e-103;
Score 1321; DB 2;
Pred. No. 2.2e-103;
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R;Cannon, P.M.; Strike, P. Plasmid 27, 220-230, 1992 Plasmid 27, 220-230, 1992 A;Title: Complete nucleotide sequence and gene organization A;Reference number: JQ1538; MUID:92383313; PMID:1325061 A;Accession: JQ1546
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C; Superfamily: be
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A; Residues: 1-286 < CAN>
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SQATMDERNRQIAEIGASLIKHW
                                               QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGYSGIIAALGPDGKPSRIVVIYTTG
                                                                                                                KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPAAMATTLRKLLTGELLTLASRQ
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                                                                                                                                                                                                                                                                                                                           97.7%;
97.7%;
                                                                                                                                                                                                                                                                                                           Score 1317; DB 2;
Pred. No. 4.7e-103;
1; Mismatches 5;
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RBSULT 11 \$00464 beta-lactamase (EC 3.5.2.6) class A - Escherichia coli plasmid p453 N;Alternate names: beta-lactamase PIT-2; beta-lactamase SHV-1 C;Species: Escherichia coli

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A;Molecule type: DNA
A;Residues: 1-30,'L',32-286 <LEE>
A;Residues: 6B:X62115; NID:948988; PIDN:CAA44025.1; PID:948990
A;Experimental source: plasmid BWH77
C;Genetics:
                                                                                                                                                                                           A;Title: Direct involvement of IS26 in an antibiotic resistance operon. A;Reference number: A35395; MUID:90264317; PMID:2160941 A;Accession: A35395
                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-286 <POD>
A;Cross-references: EMBL:X53817; NID:g43795; PIDN:CAA37813.1; PID:g43796
A;Experimental source: plasmid pZMP1
R;Lee, K.Y.; Hopkins, J.D.; Syvanen, M.
J. Bacteriol. 172, 3229-3236, 1990
                                                                                                                                                                                                                                                                                                                                                   C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 15-Oct-1999 C;Accession: S16146; A35395; S18767 R;Podbielski, A; Schoenling, J; Melzer, B.; Warnatz, K.; Leusch, H.G. J. Gen. Microbiol. 137, 569-578, 1991 A;Title: Molecular characterization of a new plasmid-encoded SHV-type beta-A;Reference number: S16146; MUID:91237320; PMID:2033379 A;Accession: S16146
                                                                                                                                                                                                                                                                                                                                                                                                                              beta-lactamase (EC 3.5.2.6) 2A precursor -
N;Alternate names: beta-lactamase SHV2A
C;Species: Klebsiella pneumoniae
C;Date: 21-Nov-1993 #sequence revision 10-N
C;Accession: S16146; A35395; S18767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Barthelemy, M.; Peduzzi, J.; Labia, R.
Biochem. J. 251, 73-79, 1988
A;Title: Complete amino acid sequence of p453-plasmid-mediated
A;Reference number: S00464; MUID:88268817; PMID:3260490
A;Accession: S00464
A;Molecule type: protein
A;Residues: 1-265 <BAR>
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                                                 ;Genome: plasmid
;Superfamily: beta-lactamase I
;Keywords: antibiotic resistan
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;Superfamily: beta-lactamase I
;Keywords: antibiotic resistance; hydrolase
                                                                                                                                                                                                                                                                                                                                    Status: preliminary; translation not shown
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Best Local
                                                                                               Gene: blaS2A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QATMDERNRQIAEIGASLIKHW 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGFX 121
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                                                   resistance; hydrolase
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   69.3%;
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Pred. No. 4.2e-71;
Score 934; DB 2;
Pred. No. 6.8e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263
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                Length
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C;Species: Escherichia
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                                                   RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-286 < GAR>
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                                                                                               PASMAERNOQIAGIGAALIEHW
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   .2.6)
coli
                   SHV-2
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                   ı
                   Escherichia
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Antimicrob. Agents Chemother. 34, 1444-1446, 1990
A; Title: Nucleotide sequence of SHV-2 beta-Lactamase gene.
A; Reference number: A60679; MUID:90351141; PMID:2201259
A; Status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: Beta-lactamase I
C;Keywords: antibiotic resistance; hydrolase
F;1-21/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: not compared with conceptual translation
                                                                                                                                                                       122 ELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLJTGELLTLASRQQ 181
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                                                                                                                                                                                                                                            GQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGFK 121
                                                                                                                                GLTAFLRQIGDNVTRLDRWETELNEALPGDARDTTTPASMAATLRKLLTSQRLSARSQRQ
                                         LIDWMEADKVAGPLLRSALPAGWPIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGS
                                                                                                                                                                                                                     GDEQLERKIHYRQQDLVDYSPVSEKHLADGMTVGELCAAAITMSDNSAANLLLATVGGPA 142
                                                                                                                                                                                                                                                                                                                                             PETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRIDA 61
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                                                                                                                                                                                                                                                                                                          PQPLEQIKQSESQLSGRVGMIEMDLASGRTLTAWRADERFPMMSTFKVVLCGAVLARVDA
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                                                                                                                                                                                                                                                                                                                                                                                                                      69.3%; Score 934; DB 2; Length 286; 67.6%; Pred. No. 6.8e-71;
                                                                                                                                                                                                                                                                                                                                                                                                 38; Mismatches
263
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A,Title: Single amino acid substitution between SHV-1 beta-lactamase and cefotaxime-hydra, Reference number: S02434; MUID:88196385; PMID:3129309
A,Accession: S02434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Huletsky, A.; Couture, F.; Levesque, R.C.
Antimicrob. Agents Chemother. 34, 1725-1732, 1990
A;Title: Nucleotide sequence and phylogeny of SHV-2 beta-lactamase.
A;Reference number: A44998, MUID:91136192, PMID:2285285
A;Accession: A44998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: beta-lactamase I
C;Keywords: antibiotic resistance; hydrolase
                                                                                                                                                                                                                                                                                                                                                                          R;Podbielski, A.; Melzer, B.
Nucletic Acids Res. 18, 4916, 1990
A;Tille: Nucleotide sequence of the gene encoding the SHV-2 beta-lactamase (bla(SHV-2))
A;Reference number: S12703; MUID:90370479; PMID:2395654
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-286 <HUL>
A;Cross-references: UNIPROT:p14558; GB:M95179; NID:g150488; PIDN:AAA25526.1; PID:g150488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 1-265 <BAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         beta-lactamase (EC 3.5.2.6) SHV-2 - Klebsiella ozaenae plasmid pBP60
C;Species: Klebsiella ozaenae
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                                                                                                                                                                          ;Genome: plasmid
;Superfamily: Beta-lactamase I
;Keywords: antibiotic resistan
                                                                                                                                                                                                                                                                  ;Cross-references:
                                                                                                                                                                                                                                                                                                                                   Status: translation not shown
                                                                                                                                                                                                                                                                                                            Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004;
Accession: A44998; S12703
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LLQWMVDDRVAGPLIRSVLPAGWFIADKTGASERGARGIVALLGPNNKAERIVVIYLRDT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIDWMEADKVAGPILRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGS 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POPLEQIKLSESQLSGRVGMIEMDLASGRTLTAWRADERFPWMSTFKVVLCGAVLARVDA 61
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                                                                                69.0%; Score 930; DB 1; ilarity 67.6%; Pred. No. 1.5e-70; Conservative 38; Mismatches 47
                                                                                                                                                                                                                                                                    EMBL: X53433; NID: g43789; PIDN: CAA37524.1; PID: g43790
                                                                                                                                                                             resistance; hydrolase
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; Pred. No. 1.3e-70;
38; Mismatches 47
                                                                                       47;
                                                                                                                              Length 286;
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263 PASMAERNQQIAGIGAALIEHW 284
                                                                                                                                                                                              242 QATMDERNRQIABIGASLIKHW 263
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Search completed: June 10, 2005, 10:58:44
Job time: 20.1791 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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3: geneseqp2090s:*
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5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
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SUMMARIES

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		Adr70416 Vector pA	Adr70404 Vector pA	Adr70410 Vector pA	Adr70422 Vector pA	Cloning	Abp55474 Vector pC	Aau75551 celZ inte	Aab31173 Amino aci	Aab50898 Protein e	Aab10440 Expressio	Aab10438 Expressio		Aay08529 Vector pA	Aaw18679 Secretory	Aaw16635 Beta-lact	Aar96423 Cytochrom		Aar31575 Ampicilli	Aaw18680 Intracell	Aaw16634 Beta-lact	Adj67709 Escherich	Aab36692 Escherich	Aae05544 B. coli m	Description	•

16-JAN-2001; 2001WO-US001651

19-JUL-2001. WO200151629-A2

13-JAN-2000; 2000US-0175968P. 15-MAR-2000; 2000US-00526106.

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26
1343	1343	1343	1343	1343	1347	1347	1347	1347	1347	1348	1348	1348	1348	1348	1348	1348	1348	1348	1348
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Escherich	RTEM with	Escherich	E. coli F	E. coli F	Amino aci	Vector pc	Human G p	E coli cl	Escherich	Recombina	Recombina	. Plasmid p	Plasmid p	Single st	Beta-lact	. hCG beta-	. Membrane	Beta-lact	Human 1mm

ALIGNMENTS

RABSULT 1
AAB05A
AAB05A
XX AAB0
XX AAB0
XX AAB0
XX AAB0
XX Inte
XX Inte
XX Inte
XX Circ
XX Cir Cleavage-site Cleavage-site Cleavage-site Active-site Cleavage-site Cleavage-site Cleavage-site Escherichia coli. Interaction-dependent enzyme association; IdBA system; biosensor; circularly permutated interaction-activated protein; marker protein; type A beta-lactamase; TRM-1 beta-lactamase; protein-protein interaction; therapeutic; drug screening; thioredoxin; ampicillin resistance. AAE05544 standard; protein; Cleavage-site Region Cleavage-site Region E. coli mature TEM-1 beta-lactamase 24-SEP-2001 AAE05544; (first entry) /note= "Inter-sub-domain loop"
190. .191 Location/Qualifiers 27. .28 149. .150 /note= "Inter-sub-domain loop" 38. .39 note= "Break-point note= note= "Break-point between alpha 'note= note= note= "Break-point between alpha note= .40 .173 .204 . 203 . 229 "Break-point between alpha "Break-point between alpha and omega fragments" "Break-point between alpha "Break-point between alpha "Break-point between alpha 263 B between alpha and and and and and and and omega omega omega omega omega omega fragments" omega fragments" fragments" fragments" fragments" fragment's" fragments"

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CC (IdEA) systems that comprises a fusion sequence that encodes for a CC circularly permutated, interaction-activated proteins that reassemble to CC form functionally reconstituted marker proteins which produce a CC detectable signal upon the association of two oligopeptides, or upon CC simultaneous association of two oligopeptides with a third oligopeptide. The marker protein is preferably a type A beta-lactamase, especially TEM-CC 1 beta-lactamase of Escherichia coli. The oligopeptide is a member of a CC protecome library selected from single chain antibody Fragment library, CC an antibody light chain variable region library and a peptide library, CC an antibody light chain variable region library and a peptide library, CC displayed within thioredoxin. The IdEA systems are useful for detecting CC extracellular proteins, particularly between two or three polypeptides. CC The systems are useful in selecting with a single marker protein the CC incorporation of multiple genetic traits in a host cell. In particular, CC dispnostics and prognostics, as well as in high-throughput screening CC systems for the discovery and validation of pharmaceutical targets and CC drugs. Prior systems or Selective Infective phage System, regular two-CC hybrid system or Selective Infective phage System, regular two-CC hybrid system or Selective Infective phage System, regular multiple steps between interaction and phenotype, which cause severe loss of efficiency CC due to high false positive and false negative rates. The present system or Selective phage System; regular transduction pathways, in high-throughput mapping of pair-wise protein-protein interactions within and CC cormat. The circularly permutated marker proteins comprising interaction-CC dependent enzymes find use in cell-based sensors for activation or inhibition of metabolic or signal transduction pathways, in high-throughput selection interactions within and in CC cormat. The present sequence is Bscherichia coli mature TEM-1 beta-lactamase enzyme from plasmid penalogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 263 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 38; Fig 2; 104pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
SQATMDERNRQIAEIGASLIKHW
                                                                                                                      QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG
                                                                                                                                                                                                                                KELTAFLHIMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRO
                                                                                                                                                                                                                                                                                                          KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HPETLVKVKDAEDQLGARVGY1ELDLNSGKILESPRPEERFPMMSTFKVLLCGAVLSRID
                                                                                                                                                                                                                                                                                                                                                                                        AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1348; DB 4;
Pred. No. 1.8e-132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a fragment complementation system (I) CC which comprises a first oligopeptide (OP1) containing an N-terminal CC fragment with a C-terminal break point and a second oligopeptide (OP2) CC comprising a C-terminal with a N-terminal breakpoint, in which the C and CC N terminal fragments are both derived from a marker protein (MP) and CC reassemble to form a functionally reconstituted MP. Methods from the CC present invention are used for monitoring the occurrence of protein-CC protein interactions in a sample, identifying oligopeptide interactions consumunoglobulin (Ig) variable region, for identifying interactions between two different proteomes, identifying epitopes that bind to an CC immunoglobulin (Ig) variable region, for identifying interactions between an extracellular domain of a transmembrane protein and a polypeptide, for CC egulated signal transducers, forming a enzyme complementation system for selecting simultaneous incorporation of multiple genetic elements into a cCC compound in a host who is in need of it. The present sequence represents the Bscherichia coli mature TEM-1 beta-lactam derivative of an antitumour CCC exemplification of the Present incorporation of the Scherichia coli mature TEM-1 beta-lactamase, which is used in the
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                                                                                                                                                                                                                                                                                                                                                                    Sequence 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 2; 94pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Balint RF,
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13-JAN-2000; 2000US-0175968P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli mature TEM-1 beta-lactamase protein sequence
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                                                                                                                                                                                                                                   263;
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                                                                                                                                HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60
              AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                    HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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                                                                                                                                                                                                                            Score 1348; DB 4;
Pred. No. 1.8e-132;
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25-MAY-1999; 99US-0135926P.
13-JAN-2000; 2000US-0175968P.
15-MAR-2000; 2000US-00526106.
The invention describes a fragment complementation system (1) comprising a first oligopeptide having an N-terminal fragment with a C-terminal break-point, and a second oligopeptide having a C-terminal fragment with a N-terminal break-point, where the N-terminal fragment and the C-terminal break-point, where the N-terminal fragment and the C-terminal fragment each are derived from a marker protein and reassemble to form a functionally reconstituted marker protein (1) is useful for selecting simultaneous incorporation of multiple genetic elements into a host cell, and activating a beta-lactam derivative of an anti-tumour compound in a host. The method described is useful for identifying a second oligopeptide to which a first ollgopeptide binds, involving coexpressing the first and second oligopeptides. Binding of the first oligopeptide to the second oligopeptide results in the functional reassembly of the marker protein. The method is also useful for monitoring the occurrence of protein-protein interactions in a sample;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pragment complementation system for detecting immunoglobulin epitope, has first oligopeptide containing N-terminal fragment with C-terminal breakpoint, second oligopeptide containing C-terminal fragment with N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 2; 47pp; English
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N-PSDB; ADJ67708.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SQATMDERNRQIABIGASLIKHW 263
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RESULT 4
AAW16634
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         identifying oligopeptide interactions between two different proteomes; and identifying epitopes that bind to an immunoglobulin variable region.

(I) or an expression casette (II), encoding a selectable N or C-terminal peptide, is useful for identifying interactions between an extra cellular domain of a transmembrane protein and a polypeptide, where the transmembrane protein is an immune cell protein, preferably CD40. (I) or (II) is useful for high-throughput identification of compound that inhibit phosphorylation-regulated cell signal transducers. (I) efficiently detects multiple interaction between extracellular and intracellular protein with high throughput format. This is the amino acid sequence of antibiotic resistance enzyme TEM-1 beta-lactamase that can be used as a selectable gene in the fragment complementation system of the
                                                                                                                                                                                           Key
Peptide
                                                                                                                                                                                                                                      Escherichia
                                                                                                                                                                                                                                                                             Gene directed enzyme prodrug therapy; GDEPT; virus directed enzyme prodrug therapy; VDEPT;
                                                                                                                                                                                                                                                                                                                       Beta-lactamase (including signal peptide)
                                                                                                                                                                                                                                                                                                                                                    09-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 263
                                                                  20-NOV-1995;
                                                                                             19-NOV-1996;
                                                                                                                         29-MAY-1997.
                                                                                                                                                     WO9719180-A2
                                                                                                                                                                                                                                                                                                                                                                                AAW16634;
                                                                                                                                                                                                                                                                                                                                                                                                         AAW16634 standard; protein;
                                       (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KELTAFLHNMGDHVTRLDRWEFELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KELTAFLHNMGDHVTRLDRWEPELNEAI PNDERDTTMPVAMATTLRKLLTGELLTLASRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SQATMDERNRQIAEIGASLIKHW
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                                                                  95GB-00023703
                                                                                               96WO-GB002845.
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/label= Sig_peptide
                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                    entry)
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Pred. No. 1
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                                                                                                                                                                                                                                                                                beta-lactamase; cancer;
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RESULT 5
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ID AAW1
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AC AAW1
XX Intr
XX Prod
XW Prod
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XW beta
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli beta-lactamase (AAW16634), including the signal peptide, is the expression product of a molecular chimaera, designated pCMV-BL (AAT66737), in which the beta-lactamase gene is under control of the CMV intermediate/early promoter. Vectors consisting of a transcriptional regulatory DNA sequence linked to a beta-lactamase gene can be used for enzyme prodrug therapy. Expression of the beta-lactamase in a targetted cell allows conversion of a prodrug into an agent toxic to the cell for treatment of cancer, viral (e.g. HIV) infection or inflammation.

Secretion of the enzyme has the advantage of increasing neighbouring cell
                                                                                                                   20-NOV-1995;
                                                                                                                                                                       19-NOV-1996;
                                                                                                                                                                                                                                                                                        WO9719183-A2
                                                                                                                                                                                                                                                                                                                                            Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                beta-lactamase;
                                                                                                                                                                                                                                                                                                                                                                                                                          Prodrug therapy; gene directed enzyme prodrug therapy; GDEPT; virus directed enzyme prodrug therapy; VDEPT; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Intracellularly-expressed beta-lactamase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW18680
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                                                               (GLAX ) GLAXO
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           Moore
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG
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                                                               GROUP LTD.
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                                                                                                                                                                          96WO-GB002846.
                                                                                                                                                                                                                                                                                                                                                                                                enzyme prodrug therapy; pCMV-delBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein;
           Sethna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1348; DB 2; 100.0%; Pred. No. 1.8e-132;
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The intracellular form (AAW18680) of TEM beta-lactamase is expressed by pCMV-delBL (AAT70311) in which a PCR-amplified beta-lactamase coding sequence, minus the signal sequence, is placed under control of the intermediate/early promoter of cytomegalovirus. Intracellular beta-lactamase constructs, placed under control of promoter/enhancer elements of lung-associated protein or neuroendocrine marker protein genes, can be used in novel chimaeric molecules for use in prodrug therapy of lung used in novel chimaeric molecules for use in prodrug therapy of lung
                                                                                                                                                       27-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                               CYP1A1; pRNH127; pRNH1: xenobiotics; circular;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Ampicillin resistance protein.
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04-JUN-1993
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N-PSDB; AAT70311.
                                                      (UYWA-) UNIV WAYNE STATE
                                                                                                      27-JUN-1991;
                                                                                                                                                                                                             19-JAN-1993
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cular; chimeric
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Pred. No. 1.8e-132;
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RESULT 7
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XX AAR9
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Best Local :
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                                                                                                                                                 Gene therapy; gene directed enzyme prodrug therapy; GDEPT; virus directed enzyme prodrug therapy; VDEPT; prodrug activation; cytotoxic; cytostatic; cancer; tumour; retrovirus; vector;
                                                                                                                                                                                                                    Secretory beta-lactamase.
                                                                                                                                                                                                                                                                                                                     AAR97619 standard; protein; 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 286 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            In vitro method for testing mutagenicity of a chemical - by metabolising chemical cell line consisting of transformed fibroblasts having detectable cytochrome P450 mixed function oxidase activity and detecting
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N-PSDB; AAQ36498.
                                                                                                                                    beta-lactamase;
                                                                                                                                                                                                                                                     20-AUG-1996 (first entry
   20-NOV-1995;
                                    30-MAY-1996.
                                                                   WO9616179-A1.
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ilarity 100.0%;
Conservative (
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     95WO-GB002716.
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Pred. No. 2e-132;
); Mismatches 0;
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ARRSULT 8
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                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
25-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecular chimaera for use in enzyme gene therapy - is activated in a target cell to express a secretable enzyme which cleaves a prodrug outside the cell into a cytotoxic or cytostatic agent.
                                                                                    US5525482-A
                                                                                                                                        Homo
                                                                                                                                                                                             cytochrome; metabolism.
                                                                                                                                                                                                                                                                               Cytochrome P450 (CYPIA1 construct).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR96423 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Page 57-58; 73pp; English.
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ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                       P450; metallothionein; mouse;
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Pred. No. 2e-132;
D; Mismatches 0;
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                                                                                                                                                                                                                          human; cytotoxicity; assay;
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11-JUN-1996

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                Gene directed enzyme prodrug therapy; GDEPT; virus directed enzyme prodrug therapy; VDEPT
                                                                Beta-lactamase (no signal peptide).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Testing chemicals for cytotoxicity to human by detecting gene damage - using recombinant fibroblasts transformed with cytochrome P450 gene under control of inducible promoter.
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09-DEC-1992;
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                                                                                                                                                                                                                                                               SQATMDERNRQIAEIGASLIKHW 263
                                                                                                                                                                                                                                                                                                          QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG
                                                                                                                                                                                                                                                                                                                                  QLIDWMEADKVAGPILRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG 240
                                                                                                                                                                                                                                                                                                                                                                       KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                      AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGWTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                                                                                                                                                            SQATMDERNRQIAEIGASLIKHW 286
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                                                                                                 (first entry)
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92US-00990295.
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                                                                                                                                                               protein;
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Pred. No. 26
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                   VDEPT; beta-lactamase; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli beta-lactamase (AAW16635), lacking the signal peptide, is the expression product of a molecular chimaera, designated pCMV-delBL (AAT66738), in which the beta-lactamase gene is under control of the CMV intermediate/early promoter. Vectors consisting of a transcriptional regulatory DNA sequence linked to a beta-lactamase gene can be used for enzyme prodrug therapy. Intracellular expression of the beta-lactamase in a targetted cell allows conversion of a prodrug into an agent toxic to the cell for treatment of cancer, viral (e.g. HIV) infection or
 Prodrug therapy; gene directed enzyme prodrug therapy; GDEPT; virus directed enzyme prodrug therapy; VDEPT; lung cancer; beta-lactamase; pCMV-BL.
                                                                  Secretory beta-lactamase.
                                                                                                 13-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 286 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example; Page 26; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecular chimaera for gene or virus directed enzyme prodrug therapy useful for treatment of cancer, viral infection or inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                               AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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                                                                                                                                                               standard;
                                                                                                                                                                                                                                                               SQATMDERNRQIAEIGASLIKHW 263
                                                                                                                                                                                                                                                                                                                            QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG
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Pred. No. 2e-132;
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Best Local Simi
Matches 263;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA construct for gene-directed enzyme prodrug therapy of lung cancer comprises lung- or neuroendocrine-specific promoter controlling expression of prodrug-converting enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 286 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-298118/27.
               03-AUG-1999
                                         AAY08529;
                                                                  AAY08529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 8ii; Page 26-27; 53pp; English.
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                                                                                                                                                                                                            QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG
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                                                                                                                                                         SQATMDERNRQIAEIGASLIKHW 263
                                                                                                                                                                                    QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG
                                                                                                                                                                                                                                                                                            AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                standard;
                                                                                                                                 SQATMDERNRQIABIGASLIKHW 286
                                                                                                                                                                                                                                         KELTAFLHNMGDHVTRLDRWEPELNBAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ
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/label= Mat_protein
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                                                               protein; 286
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                                                                                                                                                                                                                                                                                                                                                                                                  Score 1348; DB 2;
Pred. No. 2e-132;
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                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel tetracycline assay that uses recombinant CC prokaryotic cells comprising a luciferase gene under the transcriptional CC control of a tetracycline repressor and tetracycline promoter and CC involves the detection of luminescence emitted form the cells. The assay CC can be used to distinguish tetracycline form other microbial agents. The CC invention also describes a novel plasmid comprising either the luxCDABB CC genes, a tetracycline repressor (TetR) and a tetracycline promoter (TetA) from Th10. The tetracycline promoter (TetA) from Th10. The tetracycline assay CC method can be used for the determination of the medicine. The method can be used for the determination of the medicine. The method can be used to test cheese production, as cheese making bacteria are not cable to work in the presence of tetracycline. The method can also be used for the descentration of antibiotics in foodstuffs, CC e.g. for allergic people. The present assay method does not rely on the growth of microbes as do conventional tests, and so is much more rapid. The present assay is also more sensitive, as even a small amount of luminescence can be detected
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Firefly; luciferase; tetracycline; transcriptional control; TetR; TetA;
tetracycline repressor; tetracycline promoter; luminescence; luxCDABE;
insect; Tn10; medicine; dosage; cheese production; antibiotic; foodstuf
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 286 AA;
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(KARP/) KARP M.
(KURI/) KURITTU J.
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                                                                                                                                                                                                                                                                                                                        263;
                     241
                                                                                   181
                                                                                                                    144
                                                                                                                                                      121
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                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                          HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60
                                                                                                                                           KELTAFILHUMGDHVTRLDRWEPELNEAI PNDERDTTMPVAMATTLRKLLTGELLTLASRQ
SQATMDERNRQIAEIGASLIKHW
                                                                          QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG
                                                                                                                                                                                                                       AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                                                                                                                                                                         HPETLVKVKDAEDQLGARVGYIELDLNSGKILBSFRPEERFPMMSTFKVLLCGAVLSRID
                                                    QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG
                                                                                                                    KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRO
                                                                                                                                                                                       AGQEQLGRRIHYSQNDLVEYSPVTEXHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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                                                                                                                                                                                                                                                                                                                        Conservative
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Pred. No. 2e-132;
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264 SQATMDERNRQIAEIGASLIKHW 286

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RESULT 12
AAB10442
ID AAB10
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XX AAB10
XX AAB10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel method for the selection of monoclonal CC antibodies (MAb) which comprises (i) fusing B Jymphocytes with myeloma CC cells to produce antibody-producing hybridomas such that the antibodies CC are presented at the surface of the hybridomas by an antibody-binding CC invention also describes antibody-binding proteins (I); and (ii) binding the antibody to antigens (Ag). The CC invention also describes antibody-binding proteins (I) that comprise a CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa: CC malecule; an antibody-binding site of proteins A, G, L or LG, and the CC transmembrane domain of popers (plattelet-derived growth factor receptor) CC or CD52. The method is used to select MAb with specificity for particular antigens. MAb can be selected without separate culture of hybridomas, and CC election can be made against many antigens in a library, optionally on CC the basis of strength of affinity for a particular antigen. Complex CC mixtures of hybridomas can be used for selection, reducing the time and CC cost involved in MAb selection. This sequence represents the bla protein CC protein contained in the expression vector pSEX15G2 which contains the CC bla protein, Neo-R and protein G described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 286 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Selecting monoclonal antibodies, by expressing them on the surface of hybridomas attached to antibody-binding protein, then reaction with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAA71430.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 16; Fig 3; 22pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000-499832/45.
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                                                                                                                                                                                                                                                     1 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60
       KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 180
                                                                                                                                           AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                                                                                                                              HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 83
                                                                          AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vector pSEX15G2 bla protein
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                                                                                                                                                                                                                                                                                                                                                                                  Score 1348;
Pred. No. 26
                                                                                                                                                                                                                                                                                                                                                  Mismatches
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Query Match Best Local Similarity Matches 263; Conserv

AA,

Conservative

100.0%; Score 1348; DB 3 100.0%; Pred. No. 2e-132; ive 0; Mismatches 0

DB 3; 0

286; 0

Indels Length

Gaps

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RESULT 13
ARBIO438
ID ARBIO
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AC
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                                                              This invention describes a novel method for the selection of monoclonal CC antibodies (MAb) which comprises (i) fusing B lymphocytes with myeloma CC cells to produce antibody-producing hybridomas by an antibody-bindies CC are presented at the surface of the hybridomas by an antibody-binding protein (I); and (ii) binding the antibody to antigens (Ag). The CC invention also describes antibody-binding proteins (I) that comprise a CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa CC chain or a murine MHC (major histocompatibility complex) Class I k(k) CC molecule; an antibody-binding site of proteins A, G, L or LG, and the CC transmembrane domain of PDGFR (platelet-derived growth factor receptor) CC or CD52. The method is used to select MAb with specificity for particular CC antigens. MAb can be selected without separate culture of hybridomas, and CC selection can be made against many antigens in a library, optionally on CC the basis of strength of affinity for a particular antigen. Complex CC mixtures of hybridomas can be used for selection, reducing the time and CC cost involved in MAb selection. This sequence represents the Neo-R CC protein contained in the expression vector pSEXIII4 which contains the CC bla protein, Neo-R and protein G described in the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibody library.
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RESULT 14
AAB10440
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XX III-JA
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This invention describes a novel method for the selection of monoclonal CC antibodies (MAb) which comprises (i) fusing B lymphocytes with myeloma CC cells to produce antibody-producing hybridomas such that the antibodies CC are presented at the surface of the hybridomas by an antibody-binding CC protein (I); and (ii) binding the antibody to antigens (Ag). The CC invention also describes antibody-binding proteins (I) that comprise a CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa CC chain or a murine MHC (major histocompatibility complex) Class I k(k) CC molecule; an antibody-binding site of proteins A, G, L or LG, and the CC transmembrane domain of PDGFR (platelet-derived growth factor receptor) CC or CD52. The method is used to select MAb with specificity for particular antigens. MAb can be selected without separate culture of hybridomas, and CC selection can be made against many antigens in a library, optionally on the basis of strength of affinity for a particular antigen. Complex CC mixtures of hybridomas can be used for selection, reducing the time and CC cost involved in MAb selection. This sequence represents the bla protein
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                                                                                                                                                                                                                        Recombinant host cells useful for producing polysaccharase for degrading oligosaccharides, comprises a first heterologous polynucleotide encoding polysaccharase under control of surrogate promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glucanase; integration vector; pLO12306.
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                                                                                                                                                                            Disclosure; Page 82-83; 87pp; English
                                                                                                                                                                                                                                                                                                                                                                                                    Ingram LO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAY-1999;
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No. 2e-132;
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fermentation. The host cell contains at least one heterologous polynuclectide encoding a polysaccharase under the transcriptional control of a surrogate promoter capable of increasing expression o polysaccharase. The host cell also contains a second heterologous

expression of

the

The present sequence is given in a specification relating to a recombinant host cell suitable for simultaneous saccharification and

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                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 1348; DB 4; Length 286; Best Local Similarity 100.0%; Pred. No. 2e-132; Matches 263; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polynucleotide encoding a secretory polypeptide to facilitate the secretion of the expressed polysaccharase. The recombinant host cell is useful for producing polysaccharase which is useful for enzymatically degrading oligosaccharides such as lignocellulose, hemicallulose, cellulose, pectin or their combinations, and fermenting the product to ethanol, by simultaneous saccharification and fermentation processes. The present sequence is encoded by an integration vector which was introduced into cells to generate recombinant host cells. The vector contains a surrogate promoter from Zymomonas mobilis, the celZ gene from Erwinia chrysanthemi, resistance markers bla and tet, and Klebsiella oxytoca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 286 AA;
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                                                                            204
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                                                                                                                                                                                                                                                                                                          KELTAFUHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 203
                                                                                                                                                                                                                                AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAIIMSDNTAANLLLITTIGGP 120
                                                                                                QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG 240
                                                                                                                                                                              KELTAFIHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTIRKLLTGELLTLASRQ 180
SQATMDERNROIAEIGASLIKHW 286
                          SQATMDERNRQIAEIGASLIKHW 263
                                                                            QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG 263
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Search completed: June 10, 2005, 10:49:09 Job time: 103.972 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq length:
seq length:
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Match Length
          US-10-668-778-2
1348
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-08-339-658-2
US-09-233-933-7
US-09-233-933-14
US-09-253-933-21
US-09-25-769B-362
US-09-919-901-7
US-09-919-901-11
US-09-919-901-21
US-09-919-911-3-265
US-09-490-070A-362
US-09-490-153-362
US-09-490-153-362
US-09-490-153-362
US-09-490-153-362
US-09-490-324-365
US-09-490-324-365
US-09-025-769B-390
US-09-490-070A-285
US-09-490-070A-285
US-09-490-070A-285
US-09-490-070A-390
US-09-490-070A-390
US-09-490-070A-390
US-09-490-070A-390
US-09-490-070A-395
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Sequence 2, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 14, Appl
Sequence 265, App
Sequence 362, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 21, Appli
Sequence 255, App
Sequence 265, App
Sequence 362, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 265, App
Sequence 27, Appli
Sequence 27, Appli
Sequence 285, App
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US-07-721-775A-2
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                                                                                                          Matches 263;
                                                                                                                               Query Match
Best Local (
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CITY: Troy
STATE: Mich
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Database

Maximum Minimum

DB DB

Searched:

Scoring table: Sequence: Perfect score: Run on:

Regult No.

Score

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1343	1347	1347	1347	1347	1348	1348	1348	1348	1348	1348	1348	1348	1348	1348	1348	1348	1348
99.6	99.9	99.9	99.9	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
263	1293	1293	286	286	2307	2307	2307	2307	2307	2307	2307	2307	2307	299	299	299	299
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US-08-407-544-2	US-09-364-425B-57	US-09-170-496D-292	US-10-231-013-9	US-09-555-510B-9	US-10-191-966-16	US-10-191-966-9	US-10-191-966-2	US-09-919-901-16	US-09-919-901-9	US-09-919-901-2	US-09-263-933-16	US-09-263-933-9	US-09-263-933-2	US-09-490-324-300	US-09-490-324-298	US-09-490-324-285	US-09-490-153-300
Sequence 2, Appli	Sequence 57, Appl	Sequence 292, App	Sequence 9, Appli	Sequence 9, Appli	Sequence 16, Appl	Sequence 9, Appli	Sequence 2, Appli	Sequence 16, Appl	Sequence 9, Appli	Sequence 2, Appli	Sequence 16, Appl	Sequence 9, Appli	Sequence 2, Appli	•	•	Sequence 285, App	Sequence 300, App

ALIGNMENTS

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COMPUTER: IBM PC_COMPATIBLE
COMPUTER: IBM PC_DOS/MS_DOS
OPERATING SYSTEM: PC_DOS/MS_DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/721,775A
FILING DATE: 19910627
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOhm, Kenneth I.
REGISTRATION NUMBER: P-321WSU
REFERENCE/DOCKET NUMBER: P-321WSU
TELECOMOUNICATION: 1890-4071
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYLER: AMTON ACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/07721775A Patent No. 5180666 GENERAL INFORMATION:
                                                                                                                                                                                             LENGTH: 286 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: States, J. Christopher
APPLICANT: Hines, Ronald N.
APPLICANT: No. 5180666ak, Raymond F.
TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Reising, E
STREET: P.O. Box 4390
Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U.S.A.
                                                                                    Conservative
                                                                                                                                                                                           protein
                                                                                    100.0%; Score 1348; DB 1; 100.0%; Pred. No. 5.2e-141; tive 0; Mismatches 0;
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                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-339-658-2
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US-08-339-658-2
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Patent No.
                                                                                                                                                     Query Match 100.0%; Score 1348; DB 1; Length Best Local Similarity 100.0%; Pred. No. 5.2e-141; Matches 263; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,295
FILING DATE: 09-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-321MSU
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: States, J. Christopher
APPLICANT: Hines, Ronald N.
APPLICANT: No. 5525402ak, Raymond F.
APPLICANT: No. 5525402ak, Raymond F.
TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL
                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (313) 689-4071 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYDE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,658
FILING DATE: 15-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                             TOPOLOGY:
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ZIP: 48099
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    Application US/08339658
    5525482

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                                                                            HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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                  AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                   HPETLVKVKDAEDQLGARVGY1ELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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P.O. Box 4390
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                                                                                                                                                         Indels
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; SEQ ID NO 7; LENGTH: 286; TYPE: PRT; ORGANISM: Artificial Sequence US-09-263-933-7
; Sequence 14, Application US/09263933
; Patent NO. 6280940
; GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
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US-09-263-933-7
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US-09-263-933-14
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Potts, Karen E
APPLICANT: Jackson, Rober
APPLICANT: Patick, Amy K.
                                                                                                                                                                                                                                                                           264
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GENERAL INFORMATION:

APPLICANT: POCTO, ROBERTA L.

APPLICANT: POCTO, ROBERTA L.

APPLICANT: PACKON, REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A

FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/09/263,933

CURRENT FILING DATE: 1999-03-08

EARLIER APPLICATION NUMBER: 09/129,611

EARLIER APPLICATION DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PATENCIAL CONTROL

SEQ ID NO 21

LENGTH: 286

TYPE: PRI

TYPE: PRI
TYPE: PRI
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; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-263-933-14
                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
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Best Local Similarity 100.0%;
Matches 263; Conservative C
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CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
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KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 180
                                                                                                                 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTTIGGP 120
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                                                                 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 143
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Pred. No. 5.2e-141;
0; Mismatches 0;
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; MOLECULE TYPE:
US-09-025-769B-265
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                                                                                                                                                                                                              Matches 263;
                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
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APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: James F. Haley, Jr., Esq. STREET: 1251 Avenue of the Americas CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARD: PS-COLT-
                                                                                                                                                                                                                                                                                                                                    TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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                      KELTAFIHNMGDHVTRIDRWEPELNEAIPNDERDTTMPVAMATTIRKILTGELLTLASRQ 180
                                                                                                       AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                    AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 143
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 KELTAFLHNMGDHVTRLDRWEPELNEAI PNDERDTTMPVAMATTLRKLLTGELLTLASRQ
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                                                                                                                                                                                                          Score 1348; DB 3;
Pred. No. 5.2e-141;
; Mismatches 0;
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US-09-025-769B-362
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                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 1348; DB 3; Length 286; Best Local Similarity 100.0%; Pred. No. 5.2e-141; Matches 263; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 362: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Protein/(Poly)peptide libraries
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Y: USA
QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG 240
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1251 Avenue of the Americas
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Ge, Liming
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US-09-919-901-7
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 7
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                Sequence 14, Application US/09919901
Patent No. 6599738
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Patent No. 6599738
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APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR PILING DATE: 1998-08-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEO ID NOS: 33
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GENERAL INFORMATION:

APPLICANT: POCTS, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: PATICK, Amy K.

APPLICANT: PATICK, Amy K.

ITILE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-005A

FILE REFERENCE: 0125-005A

CURRENT APPLICATION NUMBER: US/09/919,901

CURRENT FILING DATE: 1090-02-08

PRIOR APPLICATION NUMBER: 09/263,933

PRIOR FILING DATE: 1999-02-08

PRIOR PILING DATE: 1999-08-05

NUMBER OF SEQ ID NOS: 33

SOPTWARE: Patentin Ver. 2.0

SEQ ID NO 21

TENTAL 206
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PRIOR PILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
PERTURE:
PERTURE:
                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Artificial Sequence
; PEATURE:
; OTHER INFORMATION: :
US-09-919-901-21
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US-09-919-901-21
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Patent No. 6599738
                                                                              Matches
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Best Local (
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Best Local Similarity
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                                                                            Local Similarity
nes 263; Conserv
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                         HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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ilarity 100.0%;
Conservative (
                                                                        100.0%; Score 1348; DB 4; Length 286; llarity 100.0%; Pred. No. 5.2e-141; Conservative 0; Mismatches 0; Indels 0
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Pred. No. 5.2e-141;
D; Mismatches 0; Indels 0
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LENGTH: 286 amino acids
TYPB: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-490-070A-265
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                                                                      Query Match
Best Local S
Matches 263
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Patent No. 6696248
GENERAL INFORMATION:
                                                                                                                                                                                                                                                         TELEPHONE: (202) 912-20:
TELEPAX: (202) 912-20:
INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
                                                                        Local Similarity
nes 263; Conserv
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: EP 95 11 3021.0 FILING DATE: 18-AUG-1995 ATTORNEY JAGENT INFORMATION:

NAME: Colin G. Sandercock, Esq. REGISTRATION NUMBER: 31,298 REFERENCE/DOCKET NUMBER: 37629-0005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 24-Jan-2000 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Knappik, Achim
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 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 83
                       HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                    100.0%; Score 1348; DB 4; ilarity 100.0%; Pred. No. 5.2e-141; Conservative 0; Mismatches 0;
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Ilag, Vic
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                                                                                                             Length
                                                                          Indels
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RESULT 12
US-09-490-070A-362
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                                                                          Matches 263;
                                                                                                            Query Match
                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 362: SEQUENCE CHARACTERISTICS: LENGTH: 286 amino acids
                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
                                                                                            Local Similarity
                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 362:
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PlueCkthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
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                  HPETLYKYKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
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White & McAuliffe
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                                                                            Conservative
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Ilag, Vic
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                                                                                          Score 1348; DB 4;
Pred. No. 5.2e-141;
                                                                          Mismatches
                                                                                                              Length
                                                                            Indels
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; LENGTH: 286 amino acids
; TYPE: amino acid
; TYPE: amino acid
; TYPE: protein
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-490-153-265
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US-09-490-153-265
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Patent No. 6706484
GENERAL INFORMATION:
                                                            Query Match
Best Local Similarity
Matches 263; Conserv
                                                                                                                                                                                                                                                                                    TELEPHONE: (212)596-900
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 265:
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: US/09/025,769B
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:

NUMBER: TEP 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                          NAME: James F. Haley, Jr., I
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MOI
TELECOMMUNICATION INFORMATION:
TELEPHONE; (212)596-9000
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Moroney, Simon
Plueckthun, Andreas
IITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSE: James F. Haley, Jr., Esq. c/o Fish &
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10021
COMPUTER READABLE FORM:
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1 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60
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                                                            100.0%; Score 1348; ilarity 100.0%; Pred. No. 5. Conservative 0; Mismatches
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RESULT 14
US-09-490-153-362
IS-09-490-153-362
; Sequence 362, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
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                                                                                                     US-09-490-153-362
                                          Query Match
Best Local Similarity
                                 Matches 263; Conservative
                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 362: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/490,153
APPLICATION NUMBER: US/09/025,769B
APPLICATION NUMBER: US/09/025,769B
APPLICATION NUMBER: US/09/025,769B
APPLICATION NUMBER: EP 95 11 3021.0
PILING DATE: 18-FBB-1998
APPLICATION NUMBER: EP 95 11 3021.0
PILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELEPHONE: (212)596-9090
TELEPAX: (212)596-9090
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq.
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 362:
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TITLE OF INVENTION: Protein/(Poly)peptide libraries
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1 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60
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                                                                                                                                                                    TYPE: amino acids
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Ilag, Vic
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                                Score 1348; DB 4;
Pred. No. 5.2e-141;
); Mismatches 0;
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Search completed: June 10, 2005, 11:01:13
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; FEATURE:
; OTHER INFORMATION:
US-10-191-966-7
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US-10-191-966-7
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SEQ ID NO 7
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

APPLICANT: Patick, Amy K.

APPLICANT: Patick, Amy K.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A

CURRENT PAPLICATION NUMBER: US/10/191,966

CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR PILING DATE: 1999-03-08
PRIOR PILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

CONTANDE SECULTARIAN OF SEQ ID NOS: 33
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SQATMDERNRQIABIGASLIKHW
                                SQATMDERNRQIAEIGASLIKHW 263
                                                                                              QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG
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Job time : 27.9646 secs

Page 8

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/AB_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfīles1.pep:*
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2005 Compugen Ltd.
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     US-07-721-775A-2
US-08-339-658-2
US-09-263-933-14
US-09-263-933-21
US-09-263-933-21
US-09-263-769B-362
US-09-919-901-7
US-09-919-901-7
US-09-919-901-71
US-09-490-070A-265
US-09-490-153-265
US-09-490-153-362
US-09-490-153-362
US-09-490-153-362
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US-09-490-070A-285
US-09-490-070A-298
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Sequence 2, Appli
Sequence 7, Appli
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Sequence 14, Appl
Sequence 265, App
Sequence 362, Appl
Sequence 14, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 21, Appli
Sequence 265, App
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Sequence 27, Appli
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	S-09-490-153-300 S-09-490-324-285 S-09-490-324-298 S-09-263-933-2 S-09-263-933-16 S-09-919-901-2 S-09-919-901-16 S-09-919-901-16 S-09-919-901-16 S-09-919-901-16 S-09-919-901-16 S-08-719-697-2 S-08-719-697-2 S-08-719-697-4 ALIGNMENTS	SDQLGARVG	100.0%; 100.0%; ive	PROMATION 589-3554 9-4071 NO: 2: FICS: acids	MARRY. 1	e St. sk	2 3S: 3, Ething 1390	J. Christ onald N. 566ak, Ra METHOD A	IIS/07721	**************************************	4

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AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120

ÁGQEÓLGRRÍHYSÓNDLVEYSÞVTEKHLTDGMTVRELCSÁAITMSDNTÁÁNLLLTTIGGÞ 143

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RESULT 3
US-09-263-933-7
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US-08-339-658-2
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Best Local Similarity
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Patent No. 5525482
                                                                                                                                                                                                                                                                                                         Matches
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APPLICANT: States, J. Christopher
APPLICANT: Hines, Ronald N.
APPLICANT: No. 5525482ak, Raymond F.
TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (313) 689-4071
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TYPE: amino acid
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APPLICATION NUMBER: US 07/990,295
FILING DATE: 09-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,658
FILING DATE: 15-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Reising, 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (313) 689-3554
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CITY: Troy
STATE: Mich
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REFERENCE/DOCKET NUMBER: P-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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                                                                                                KELTAFLHNMGDHVTRLDRWEPELNEAIP 149
                                                                                                                                                                         AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
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                                                                                                                                                     AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 143
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US-09-263-933-14
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; ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A CURRENT APPLICATION NUMBER: US/09/263,933 CURRENT FILING DATE: 1999-03-08 EARLIER APPLICATION NUMBER: 09/129,611 EARLIER FILING DATE: 1998-08-05 NUMBER OF SEQ ID NOS: 33 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/09263933 Patent No. 6280940
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Best Local Similarity
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APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                            ENGTH: 286
                                                                                                                                                                          149;
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                        61 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
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                                                                                       HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 143
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100.0%; Pred. No. 2.9e-84;
tive 0; Mismatches 0;
                                                                                                                                                                                                                   Length 286;
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KELTAFLHNMGDHVTRLDRWEPELNEAIP 149

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TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
FEARLIER APPLICATION NUMBER: 09/129,611
FEARLIER APPLICATION NUMBER: 09/129,611
FEARLIER FILING DATE: 1998-08-05
NUMBER: OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
FENOTH: 286
TYPE: PAT
ORGANISM: Artificial Sequence
US-09-263-933-21
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Best Local Similarity
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Patent No. bzuc-
Patent INFORMATION:
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APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
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APPLICANT:
APPLICANT:
         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
                                                                                                                                                                                                                                                                                                      APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                    STREET: 1251 Ave
CITY: New York
STATE: New York
                                                                                                                                                                             ZIP: 10021
                                                                                                                                                                                           COUNTRY:
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5. 630006
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Ilag, Vic
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18-FEB-1998
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RESULT 7
US-09-025-769B-362
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APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION UNMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
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LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
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REFERENCE/DOCKET NUMBER: MC
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Ilag, Vic
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INFORMATION FOR SEQ ID NO:

362:

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APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/09/919,901

CURRENT FILING DATE: 2001-08-02

PRIOR APPLICATION NUMBER: 09/263,933

PRIOR FILING DATE: 1999-02-08

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 7

INWEST OF SEQ ID NOS: 33
US-09-919-901-14
; Sequence 14, Application US/09919901
; Patent No. 6599738
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; OTHER INFORMATION: :
US-09-919-901-7
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Best Local S
Matches 149
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Best Local Similarity 100.
Matches 149; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 286
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                                                                                                                                        KELTAFLHNMGDHVTRLDRWEPELNEAIP 172
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RESULT 10
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APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
APPLICANT: PATICN: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT FAPPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR PILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
CONTROL OF SEQ ID NOS: 33
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CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
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APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Potts, Karen E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
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y Match 100.0%; Score 770; DB 4; Local Similarity 100.0%; Pred. No. 2.9e-84; O; Mismatches 0;
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149; Conserv
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RESULT 11
US-09-490-070A-265
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                  Query Match 100.0%; Score 770; DB 4; Length 286; Best Local Similarity 100.0%; Pred. No. 2.9e-84;
                                                                                                                                                                                                                               Matches 149; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Versi
CURRENT APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
APPLICATION NUMBER: 31,298
NAME: COlin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 265:
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                                                                                                                                                                       HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60
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KELTAFLHNMGDHVTRLDRWEDELNEAIP 149
                                                                                                                                           HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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TYPE: amino acid
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Plueckthun, Andreas
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Ilag, Vic
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US-09-490-070A-362
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    ; Sequence 265, Application US/09490153 ; Patent No. 6706484 ; GENERAL INFORMATION:
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                                                                                       RESULT 13
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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MEDGIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
PRIOR APPLICATION NUMBER: 31,298
ATTORNEY/AGENT INFORMATION:
NAME: COlin G. Sandercock, Esq.
REGERENCENDOCKET NUMBER: 37,629-0005
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 362.
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                                                                                                                                                                                    KELTAFLHNMGDHVTRLDRWEPELNEAIP 149
                                                                                                                                                                                                                                 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 143
                                                                                                                                                                                                                                                                                                                  HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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COUNTRY: USA
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White & McAuliffe
                                                                                                                                                    KELTAFLHIMGDHVTRLDRWEPELNEAIP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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Plueckthun, Andreas
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83

Moroney, Simon Plueckthun, Andreas

Ge, Liming

Peter

NUMBER OF SEQUENCES: 373

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RESULT 14
US-09-490-153-362
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                                                                                                                                                              Sequence 362, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
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Best Local Similarity
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TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 265:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Protein/(Poly)peptide libraries NUMBER OF SEQUENCES: 373
             TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein SEQ ID NO: 265:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 770; DB 4; ilarity 100.0%; Pred. No. 2.9e-84; Conservative 0; Mismatches 0;
Moroney, Simon
Plueckthun, Andreas
INVENTION: Protein/(Poly)peptide libraries
                                                                                                                                            Knappik, Achim
                                                                                                Trag,
                                                                                                                     Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 286;
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; TOPOLOGY: locate
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 362:
US-09-490-153-362
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US-10-191-966-7
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                        APPLICANT: POTTE, KATEN E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: PATICK, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/10/191,966

CURRENT FILING DATE: 2002-07-10

PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR FILING DATE: 1999-03-08

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR PILING DATE: 1998-08-05

PRIOR FILING DATE: 1998-08-05
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (212)596-9090 INFORMATION FOR SEQ ID NO: 362:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
COMPUTER PLADABLE FLOPPY disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: EP 95 11 3021.0 FILING DATE: 18-AUG-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acids
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CITY: New York
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100.0%; Pred. No. 2.9e-84;
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Result
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Match
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1: /cgm2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgm2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgm2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgm2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgm2_6/ptodata/1/iaa/backfIles1.pep:*
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Gapop 10.0 ,
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Copyright (c) 1993 - 2005 Compugen Ltd.
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 US-07-721-775A-2
US-08-339-65B-2
US-08-339-33-14
US-09-263-933-21
US-09-263-933-21
US-09-263-931-21
US-09-919-901-7
US-09-919-901-21
US-09-919-901-21
US-09-490-070A-265
US-09-490-153-362
US-09-490-153-362
US-09-490-153-362
US-09-490-153-362
US-09-490-153-362
US-09-490-153-362
US-09-490-153-362
US-09-490-153-285
US-09-025-769B-285
US-09-490-070A-285
US-09-490-070A-285
US-09-490-070A-285
US-09-490-070A-298
US-09-490-070A-298
US-09-490-070A-396
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Sequence 2, Appli
Sequence 1, Appli
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Sequence 11, Appli
Sequence 21, Appli
Sequence 365, App
Sequence 362, Appli
Sequence 21, Appli
Sequence 265, App
Sequence 362, App
Sequence 362, App
Sequence 362, App
Sequence 11, Appli
Sequence 11, Appli
Sequence 21, Appli
Sequence 285, App
Sequence 298, App
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1 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 	Match 100.0%; Score Local Similarity 100.0%; Pred. es 228; Conservative 0; Mism) Z	APPLICATION NUMBER: US/07/21,/75A FILING DATE: 19910627 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Kohn, Kenneth I. REGISTRATION NUMBER: 30,955 REGISTRATION NUMBER: P-321WSU TREFORMATION INFORMATION:	: disk disk cros/ms-pos cros/ms-pos Release #1.0, TA:	DRWATION: States, J. Christopher: Hines, Ronald N. No. 5180666ak, Raymond INVENTION: METHOD AND CE INVENTION: METHOD AND CE INVENTION: MUTAGENICITY SEQUENCES: 2 DENCE ADDRESS: EE: Reising, Ethington, p.O. Box 4390	ALIGNMENTS SULT 1 -07-721-775A-2 Sequence 2, Application US/07721775A Datent No. 518666	1170 100.0 299 4 US 1170 100.0 299 4 US 1170 100.0 299 4 US 1170 100.0 299 3 US 1170 100.0 2307 3 US 1170 100.0 2307 3 US 1170 100.0 2307 4 US 1169 99.9 286 4 US 1169 99.9 1293 4 US 1169 99.9 1293 4 US
GKILESFRPEERFPMMSTFK 	DB 1; Length 7e-122; 0; Indels			Version #1.25	F. LL LINE FOR TESTING OF A CHEMICAL Barnard, Perry & Milton	ENTS	324 285 324 298 324 300 33 - 3 933 - 9 933 - 16 933 - 16 934 - 2 956 - 2 966 - 2 966 - 2 966 - 2 966 - 16 966 - 2 966 -
VLLCGAVLSRID 60	286; 0; Gaps 0,				-		Sequence 300, App Sequence 285, App Sequence 298, App Sequence 300, App Sequence 2, Appli Sequence 9, Appli Sequence 16, Appli Sequence 9, Appli Sequence 16, Appli Sequence 2, Appli Sequence 16, Appli Sequence 9, Appli Sequence 27, Appli Sequence 27, Appli

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                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,295
FILING DATE: 09-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REGISTRATION NUMBER: 30,955
                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (313) 689-407
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,658
FILING DATE: 15-NOV-1994
                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 689-3554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: States, J. Christopher
APPLICANT: Hines, Ronald N.
APPLICANT: No. 552548284, Raymond F.
TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Reising, Ethington, Barnard, Perry & Milton STREET: P.O. Box 4390
                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Michigan
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                          KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 180
                                                                                                                          AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                                                                                    HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 83
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                                                                                  AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (313) 689-4071
(317) TD NO: 2:
                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                            DB 1; Length 286;
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RESULT 4
US-09-263-933-14
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; ORGANISM: Artificial Sequence US-09-263-933-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT;
TITLE OF INVENTION: OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
                                                                      SEQ ID NO 14
LENGTH: 286
                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 6280940 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/09263933 Patent No. 6280940
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Best Local Similarity
                                                                                                                                       APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REPERSINCE: 10125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER PILING DATE: 1998-08-05
NUMBER: OF SEQ ID NOS: 33
RUMBER OF SEQ ID NOS: 33
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                                                                                                                        SOFTWARE: PatentIn Ver. 2.0
                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1170; DB 3; 100.0%; Pred. No. 6.7e-122; 0: Mismatches 0;
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Sequence 21, Application US/09263933

Patent NO. 6280940

GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Potts, Karen E.
APPLICANT: Patick, Amy K.
ITILE OF INVENTION: REPORTER GENE SYSTEM FOR TITLE OF INVENTION: OF INHIBITORS OF THE HEP.
FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/09/263,933

CURRENT FILING DATE: 1999-03-08

EARLIER APPLICATION NUMBER: 09/129,611

EARLIER FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 21

LENGTH: 286
                                                                                                         RESULT 6
US-09-025-769B-265
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                                                  Sequence 265, Application US/09025769B Patent No. 6300064 GENERAL INFORMATION:
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Best Local (
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Best Local
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APPLICANT:
APPLICANT:
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Knappik, Achim
Pack, Peter
Ilag, Vic
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RESULT 7
US-09-025-769B-362
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-265
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APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neav
                                                                                                                                                                                             ; Sequence 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
GENERAL INFORMATION:

APPLICANT: Knapplk, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Moroney, Simon
APPLICANT: Protein/(Poly)peptide libraries
NUMBER OF ENCENTION: Protein/(Poly)peptide libraries
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Best Local Similarity
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX: (212)596-9090
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                                                                                                                                                                                                                                                                                                                        204
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p. 6300064
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CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York
STATE: New York

COUNTRY:

USA

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                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/09919901 Patent No. 6599738 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 1170; DB 3; Length Best Local Similarity 100.0%; Pred. No. 6.7e-122; Matches 228; Conservative 0; Mismatches 0; Indels
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
                                                          APPLICANT: POTTS, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Pattick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212)596-9090 INFORMATION FOR SEQ ID NO: 362:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F Halov IV Rec
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: James F. Haley, Jr., I
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MOI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
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US-09-919-901-14
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LENGTH: 286
TYPE: PRI
ORGANISM: Artificial Sequence
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Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                       Local Similarity
                     181
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QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDG
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                                                           KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ
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                                                                                                                                   AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 143
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                                                                                                                                                                                                                                                                                   100.0%; Score 1170; DB 4;
100.0%; Pred. No. 6.7e-122;
tive 0; Mismatches 0;
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RESULT 11
US-09-490-070A-265
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US-09-919-901-21
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GENERAL INFORMATION:
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APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0115-0105A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21, Application US/09919901 Patent No. 6599738
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Best Local
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CURRENT FILLING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: :
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hes 228; Conserva
                                                                                                                                                                                        Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
  COMPUTER READABLE FORM:
                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Knappik, Achim
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               CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDG 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 180
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                                                                                                        STREET: 1666 K Street, N.W., Suite 300
                                                                                                                               ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe
                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09490070A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                      Ge, Liming
                                                                                                                                                                                                                                                                                                 Ilag,
                                                                                                                                                                                                                                                                                                            Pack, Peter
Ilag, Vic
                                                                                                                                                                                                                                                          Moroney, Simon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Sequence 362, Application US/09490070A
Patent No. 6695248
GENERAL INFORMATION:
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Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 265: SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
                                                             ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 265:
                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAullffe
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                 Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Knappik, Achim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDG
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX: (202)
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Ilag, Vic
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Pred. No. 6.7e-122;
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83

FILING DATE: 24-Jan-2000 PRIOR APPLICATION DATA: CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,070A

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Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
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TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 362:
                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 100.0%; Score 1170; DB 4; Local Similarity 100.0%; Pred. No. 6.7e-122; nes 228; Conservative 0; Mismatches 0;
                                                                                                                                                                                               NUMBER OF SEQUENCES: 3,3

CORRESPONDENCE ADDRESS:
Annes F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 362:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: EP 95 11 3021.0 FILING DATE: 18-AUG-1995 ATTORNEY AGENT INFORMATION: NAME: Colin G. Sandercock, Esq. REGISTRATION NUMBER: 31,298 REFERENCE/DOCKET NUMBER: 37629-0005 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Protein/(Poly)peptide libraries NUMBER OF SEQUENCES: 373
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APPLICATION NUMBER: US/09/025,769B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09490153
                                                                                                                                                                                                                                                                                                                                                                                                                       Moroney, Simon
Plueckthun, Andreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ge, Liming
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TOPOLOGY: linear

HOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-490-153-265
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US-09-490-153-362
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GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                         CORRESPONDENCE ADDRESS:

ADDRESSE: James F. Haley, Jr., Esq. c/o Fish & Neave ADDRESSE: James F. Haley and Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
CITY: New York
CITY: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025;769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
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REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Knappik, Achim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09490153
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Ilag, Vic
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NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:

ATTORNEY/AGENT INFORMATION:

```
APPLICANT: POETS, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

APPLICANT: Patick, Amy K.

ITITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

FILE REFERENCE: 0125-0005A

CURRENT FILING DATE: 2002-07-10

PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO. 76
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; OTHER INFORMATION: :
US-10-191-966-7
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                                                                                                                                                    Query Match 100.0%; Score 1170; DB 4; Length 286; Best Local Similarity 100.0%; Pred. No. 6.7e-122; Matches 228; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/10191966
Patent No. 6790612
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Best Local :
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TYPE: PRT
TYPES: PRT
ORGANISM: Artificial Sequence
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TELEPAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 362:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 362:
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61 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
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                                                                               HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60
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                                                 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 83
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Search completed: June 10, 2005, 11:01:18
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-837-306-354
US-10-191-966-14
US-10-191-966-21
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1144.220 Million cell updates/sec
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Sequence 2, Appli
Sequence 7, Appli
Sequence 14, Appl
Sequence 21, Appl
Sequence 354, Appl
Sequence 7, Appli
Sequence 14, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 73, Appl
Sequence 73, Appli
Sequence 7, Appli
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288	284	498	262	262	264	264	264	265	265	265	265	265	584	362	264	286	286	286	286	286	285	265	265	265	1967	1293	286	286	2307	2307	2307	2307	2307
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US-10-016-668-6	-10-062-188-	-10-491-653-	-10-393-449-	10-	10-656-029-	US-10-280-482-8	9-772-1	US-10-877-952-154	US-10-656-029-6	US-10-622-088-114	US-10-280-482-6	US-09-772-114-8	1	10-469-199-	10-877-952-	US-10-877-952-71	10-877-952-	10-656-029-	US-10-280-482-4	US-10-016-668-5	US-09-772-114-7	US-10-656-029-2	S-10-280-482-	0	-10-477-044-	-10-251-385-	-10-842-	-10-231-013-	-10-191-966-	-10-191-	-10-191-966-	-09-919-901-	US-09-919-901-9
6	equence 2,	146	equence 3,	Sequence 3, Appli	е 8,	e 8	9, Appli				w	Sequence 8, Appli	N	N	18	71,		4,	4	e 5,	,7	N	o N	٠,	_	2	,		equence 16,	9	equence 2,	e 16,	Sequence 9, Appli

ALIGNMENTS

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Sequence 2, Application US/10668778

| Sequence 2, Application No. US20040038317A1
| GENERAL INFORMATION:
| APPLICANT: Balint, Robert F.
| APPLICANT: Walledios, Inc.
| TITLE OF INVENTION: Interaction-Activated Proteins
| FILLE REFERENCE: 021167-000700US
| CURRENT FILING DATE: 2003-09-22
| CURRENT FILING DATE: 2003-09-25
| PRIOR APPLICATION NUMBER: US/09/526,106
| PRIOR PILING DATE: 12000-03-15
| PRIOR PILING DATE: 1999-03-15
| PRIOR PILING DATE: 1999-03-25
| PRIOR PILING DATE: 1999-05-25
| PRIOR APPLICATION NUMBER: US 60/135,926
| PRIOR APPLICATION NUMBER: US 60/175,968
| PRIOR PILING DATE: 1999-05-25
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                                                              Sequence 14, Application US/09919901 Publication No. US20030082518A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 228; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/09919901 Publication No. US20030082518A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 7
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Potts, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHISTORS OF THE HEPATITIS C VIRUS PROTEASE FILE REPERENCE: 0125-0005A

CCURRENT APPLICATION NUMBER: US/09/919,901

CURRENT FILING DATE: 2001-08-02

PRIOR APPLICATION NUMBER: 09/263,933

PRIOR FILING DATE: 1999-02-08

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR PILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
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RESULT 4
US-09-919-901-21
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                                                     Query Match
Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                    SEQ ID NO 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 228; Conserv
                                                                                                                                                                                                                                                                                                                  APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR PILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
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CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR PILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
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                                                                                                                                                                                                                                                                             LENGTH: 286
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                                                                      100.0%; Score 1170; DB 10; 100.0%; Pred. No. 9.2e-113; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1170; DB 10; 100.0%; Pred. No. 9.2e-113; tive 0; Mismatches 0;
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FILE REFERENCE: DYAX/002
CURRENT APPLICATION NUMBER: US/09/837,306
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR FILING DATE: 2000-04-17
NUMBER OF SEQ ID NOS: 428
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 354
LENGTH: 286
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Sequence 7, Application US/10191966
Publication No. US20030175692A1
GENERAL INFORMATION:
APPLICANT: Potts, Karen B.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 228; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROOKBY, KRISTIN L.
APPLICANT: HOST, RENE
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC
TITLE OF INVENTION: PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A
TITLE OF INVENTION: DIVERSE FAMILY OF PEPTIDES, POLYPEPTIDES OR PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Unknown Organism: pCESS
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Pred. No. 9.2e-113;
); Mismatches 0;
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APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/10/191,966

CURRENT FILING DATE: 2002-07-10

PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR FILING DATE: 1998-03-08

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                      ; TYPE: PRT; ORGANISM: Artificial Sequence; FEATURE: ; OTHER INFORMATION: : US-10-191-966-14
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LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                     Matches
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CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
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OTHER INFORMATION:
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                                                                                   100.0%; Score 1170; DB 14; 100.0%; Pred. No. 9.2e-113; tive 0; Mismatches 0;
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                                                                                                                            Sequence 523, Applic Publication No. US20 GENERAL INFORMATION:
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SEQ ID NO 21
LENGTH: 286
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Publication No. US20030175692A1
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APPLICANT: Jackson, Roberta L.
APPLICANT: Datick, Amy K.
APPLICANT: Patick, Amy K.
APPLICANT: PATICLS, REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE PILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1999-03-08
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
               APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROOKEY, KRISTIN L.
APPLICANT: HOET, REME
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HOOGENBOOM,
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o. US20030232333A1
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FILE REFERENCE: DYAX/002 CIP2
CURRENT APPLICATION NUMBER: US/10/045,674
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 69/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 523
LENGTH: 286
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US-10-416-708A-73
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SEQ ID NO 73
LENGTH: 286
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Best Local Similarity
Matches 228; Conserva
                                                                                Matches
                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING FITTE OF INVENTION: SPECIFICITIES FILE REFERENCE: 37779-0004
CURRENT APPLICATION UNMERS: US/10/416,708A
CURRENT FILING DATE: 2004-01-28
RUMBER OF SEQ ID NOS: 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wise, John G. APPLICANT: Fromknecht, Katja
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ORGANISM: Artificial Sequence
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                                                                          Score 1170; DB 15,
Pred. No. 9.2e-113;
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; FEATURE:
; OTHER INFORMATION: :
US-09-919-901-2
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US-09-919-901-2
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Sequence 9, Application US/09919901
Publication No. US2030082518A1
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
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Best Local Similarity 100.0%; F
Matches 228; Conservative 0;
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SEQ ID NO 2
LENGTH: 2307
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APPLICANT: Potts, Karen B.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: OF INFIELD FROM POR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INFIELTORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
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CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
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APPLICANT: Potts, Karen B.

APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/09/919,901

CURRENT FILING DATE: 2001-08-02

PRIOR APPLICATION NUMBER: 09/263,933

PRIOR FILING DATE: 1999-02-08

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 16

LENGTH: 2307
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PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
SEQ ID NO 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
COTTED INCOMMENTION.
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Publication No. US20030082518A1
GENERAL INFORMATION:
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                                                                                                                                                                                               Best Local Similarity
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ORGANISM: Artificial
FEATURE:
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                                                                            2045 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 2104
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                                                                                                                                                                  100.0%; Score 1170; DB 10; al Similarity 100.0%; Pred. No. 1.7e-111; 228; Conservative 0; Mismatches 0;
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AGGEGLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
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APPLICANT: Potts, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

APPLICANT: Patick, Amy K.

ITILE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A

FILE REFERENCE: 0125-0005A

FULL REFERENCE: 0125-0005A

FULL REFERENCE: 0202-07-10

PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR FILING DATE: 1999-03-08

PRIOR FILING DATE: 1999-03-08

PRIOR FILING DATE: 1998-08-05

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 2307

TYPE: PRI
ORGANIAM: Artificial Segmence
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US-10-191-966-9
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                                                                                                                                                                                                     Sequence 9, Application US/10191966 Publication No. US20030175692A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/10191966
Publication No. US20030175692A1
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Best Local Similarity
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                                               APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
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PRIOR APPLICATION NUMBER: 09/
PRIOR FILING DATE: 1998-08-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence FEATURE:
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2225
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                   QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDG 228
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975
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1: uniprot_sprot:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5
286	286	286	286	286	286	286	286	286	286	286	286	286	286
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Q9R770	Q9K582	Q9EYX1	Q8GA85	Q844X1	Q7DHD3	Q7DFY3	Q7BR75	Q7BP57	Q7B899	Q7B3X5	Q6WZD4	Q6WRX2	1r6M9Ö
Q9r770	Q9k582	Q9eyx1	Q8ga85	Q844x1	Q7dhd3	Q7dfy3	Q7br75	Q7bp57	Q7b899	Q7b3x5	Q6wzd4	Q6wrx2	Q6w9j1
escherichia	klebsiella	escherichia	escherichia	klebsiella	serratia ma	salmonella	neisseria m	shigella fl	klebsiella	citrobacter	acinetobact	zymomonas m	enterobacte

ALIGNMENTS

RESULT 2 Q6WWY4 ID Q6WWY4 PRELIMINARY; PRT; 232 AA. ID Q6WWY4; AC Q6WWY4; DT 05-JUL-2004 (TrEMBLrel. 27, Created) DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)	Qy 181 QLIDWMEADK 190 Db 182 QLIDWMEADK 191	Qy 121 KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTIMPVAMATTLRKLLTGELLTLASRQ	Qy 61 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP	Qy 1 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID	Query Match 100.0%; Score 975; DB 2; Length 229; Best Local Similarity 100.0%; Pred. No. 2.5e-74; Matches 190; Conservative 0; Mismatches 0; Indels 0; Ga	DR PRINTS; PROUND(1); BELG LACCIMINAGE. DR PROSITE; PS00116; BETA_LACCIMINAGE. DR PROSITE; PS00146; BETA_LACCIMINAGE. PT NON_TER 1 1 FT NON_TER 229 229 SQ SEQUENCE 229 AA; 25067 MW; C85582C2617F4467 CRC64;	SEQUENCE FROM N.A. STRAIN-MISC126; STRAIN-MISC126; Obert C.A., Goldstone C.M., Gordon I Submitted (APR-2004) to the EMBL/Ger EMBL; AY265885; AAP93843.1; HSSP; P00807; IKGE.		DT 05-JUL-2004 (TrEMBLrel. 27, Created) DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) DE Beta-lactamase (Fragment). GN Name-blaTEM;	W SU
		GELLTLASRQ 180 GELLTLASRQ 181	NLLLTTIGGP 120 NLLLTTIGGP 121	LCGAVLSRID 60	•••			iales;		

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RESULT
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STRAIN-MISC198;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=MISC112;
Obert C.A., Goldstone C.M.,
Submitted (APR-2004) to the
EMBL; AY265882; AAP93840.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON TER
                                                                                                                                                                                                                                                                                                                   HSSP; P00807; 1KGE.
InterPro; IPR001466; Beta lactamase.
InterPro; IPR000871; Beta lactamase A.
Pfam; PF00114; Beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Klebsiella.
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                                                                                                                                                                                                                                                 PRINTS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=blaTEM;
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NCBI_TaxID=569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beta-lactamase (Fragment).
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PRINTS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE_A; 1.
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232 AA;
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EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gordon D.M., Riley
EMBL/GenBank/DDBJ
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Last annotation updat
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    Score 975; DB 2;
Pred. No. 2.6e-74;
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STRAIN-TA005;
STRAIN-TA005
Obert C.A., Goldstone C.M., Go
Submitted (Apr-2004) to the EN
EMBL; AY265887; AAP93845.1;
HSSP; P00807; IKGE.
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Escherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
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NON_TER 242 242
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                                                                                                                                                                                                                                                                                                                                          AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
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                                                                                                                                                                                           QLIDWMEADK 190
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                                                                                                                                              QLIDWMEADK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242
242 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242
26554 MW;
                                                                                                                                                 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gordon D.M., Riley M.A.;
EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 975; DB 2; Pred. No. 2.6e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38C3DFA8A5A3807D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Q6KB67 Q6KB67;

PRELIMINARY;

PRT;

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RESULT 6
Q3805
ID Q380
AC Q380
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PSEQUENCE FROM N.A.

WHEDLINE-95172401; PubMed-7867948; DOI=10.1016/0378-1119(94)00839-K;

WA Henrich B., Schmidtberger B.;

WA Henrich B., CAB84692.1; -.

WA HENRY MAN H
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Best Local
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Q38058;
01-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-JUN-2003 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUB-First leaf;
Jansen C., Korell M., Eckey C., Biedenkopf D., Kogel K.H.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ717739; CAG30723.1; -.
HSSP; P00807; 1ALQ.
InterPro; IPR001466; Beta_lactamase.
InterPro; IPR000871; Beta_lactamase_A.
Pfam; PF00144; Beta_lactamase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein (Fragment).
Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteriophage phi-X174.
Viruses; ssDNA viruses; Microviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00118; BLACTAMASEA.

PROSITE; PS00146; BETA_LACTAMASE_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=bla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beta lactamase.
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NON_TER 285 28
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Last annotation update)
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Pred. No. 3.2e-74;
); Mismatches 0;
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Best Local Sim
Matches 190;
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Best Local S
Matches 190
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Q00626; O08022; O08102; O09393; O09396; O09397; O09398; O09399;
O09400; O09401; O09402; O09403; O09404; O09405; O09406; O09407;
O09408; O09481; O09482; O09483; O09490; Q57339;
O1-NOV-1996 (TYEMBLTel. 01, Last sequence update)
25-OCT-2004 (TYEMBLTel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

PLASMID=J3356/pOX7/3, and J3356/POX7/1;

PLASMID=J3356/pOX7/3, and J3356/POX7/1;

MEDLINE=96422755; PubMed=8825372; DOI=10.1006/plas.1995.0005;

MEDLINE=96422755; PubMed=8825372; DOI=10.1006/plas.1995.0005;

Needham C., Noble W.C., Dyke K.G.;

"The staphylococcal insertion sequence IS257 is active.";

"The staphylococcal insertion sequence IS257 is active.";

Plasmid 34:198-205(1995).

EMBL; U36911; AAB39956.1; -...

EMBL; U36911; AAB39956.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus.
Plasmid J3356/pOX7/3, i
Plasmid Firmicutes; l
Bacteria; Firmicutes; l
NCBI TaxID=1280;
                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001466; Beta lactamase. InterPro; IPR000871; Beta lactamase A. Pfam; PF00144; Beta-lactamase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beta-lactamase.
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                                                                                                                                                                                                                                                                                                             PRINTS; PRO0118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAM
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                                                                                                                                                                                                                        h 100.0%; So Similarity 100.0%; Po 90; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                 QLIDWMEADK 190
                                                                       KELTAFLHNMGDHVTRLDRWEPELNEAI PNDERDTTMPVAMATTLRKLLTGELLTLASRQ
                                                                                                                           AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                                                                    HPETLYKYKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                                                                                                                                                                                   HPETLYKYKDAEDQLGARVGYIELDLNSGKILESFRPBERFPMMSTFKVLLCGAVLSRID
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QLIDWMEADK 213
                                                                                                               AGQEQLGRRIHYSQNDLVEYSPVTEXHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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                                                      KELTAFIHNMGDHVTRLDRWEPELNEA I PNDERDTTMPVAMATTLRKLLTGELLTLASRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ
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                                                                                                                                                                                                                                                                                   286 AA;
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Bacillales; Staphylococcus.
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Pred. No. 3.2e-74;
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Pred. No. 3.2e-74;
; Mismatches 0;
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Best Local Similarity
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Q79CL6;
05-JUL-2004
                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Mutant extended-spectrum beta-lactamase precursor ()
Name=bla; Synonyms=blaTEM-116;
Becherichia coli
                                                                                                                                                                Escherichia coll.
Plasmid pRP4, and Plasmid pCAPs.
Plasmid profenhacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q79DR3
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InterPro; IPR001871; Beta lactamase_A.
Pfam; PF00144; Beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA LACTAMASE A; 1.
PROSITE; PS00146; BETA LACTAMASE A; 1.
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Submitted (JUL-1995) to the
EMBL; U31280; AAC44581.1;
HSSP; P00807; 1ALQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE=97074643; PubMed=8917070; DOI=10.1016/0378-1119(96)00114-X; Serebrijski I.G., Vassin V.M., Tsygankov Y.D.; "Two new members of the BioB superfamily: cloning, sequencing and expression of bioB genes of Methylobacillus flagellatum and Corynobacterium glutamicum."; Gene 175:15-22(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Methylobacillus flagellatum.
Bacteria; Proteobacteria; Betaproteobacteria; Methylophilales;
Methylophilaceae; Methylobacillus.
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05-JUL-2004
                                                 SEQUENCE
                                                                                                                                                     Bacteria; Proteobacteria;
Enterobacteriaceae; Escher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q79DR3;
                                                                                                              NCBI_TaxID=562;/
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e EMBL/GenBank/DDBJ databases
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Pred. No. 3.2e-74;
); Mismatches 0;
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Q38212;
Q1-NOV-1996 (Tr
01-NOV-1996 (Tr
01-MAR-2002 (Tr
Bacteriophage f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   produced by Clinical Isolates of Klebsiella coli from a Korean Nationwide Survey,"; J. Clin. Microbiol. 42:2902-2906(2004).

EMBL; M74750; AAA24057.1; --
EMBL; Y12694; CAA73226.1; --
EMBL; AY425988; AAQ95605.1; --
EMBL; AY425988; AAQ95605.1; --
EMBL; AY425988; AAQ95605.1; --
EMBL; P00807; IALQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0008800; F:beta-lactamase activity; GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR001466; Beta-lactamase.
InterPro; IPR000871; Beta-lactamase.
PF00144; Beta-lactamase.A.
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase; Plasmid; SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=15243036;
Jeong S.H., Bae I.K., Lee J.H.,
Kim Y.H., Jeong B.C., Lee S.H.,
"Molecular Characterization of E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98189310;
Schlieper D., Von
Mueller-Hill B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=K12; PLASMID=pRP4; Rondot S., Anthony K., Du Little M., Breitling F.;
                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00146;
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00118; BLACTAMASEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli
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Escherichia coli.";
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Submitted (AUG-1991) to the EMBI
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                                                                                                                                                                                                  KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 180
                                                                                                                                                                                                                                     AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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                                                                                                                                  QLIDWMEADK
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                                                                                                                                                                                  KELTAPLHNMGDHVTRLDRWEPELNEAI PNDERDTTMPVAMATTLRKLLTGELLTLASRQ
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                                                                                                                                                                                                                                                                                                                                                                                           286 AA;
  (TrEMMBLrel. 01, Created)
(TREMBLrel. 01, Last sequence update)
(TREMBLrel. 20, Last annotation update)
ye f1-R208 ampicillinase gene mutation.
                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=9514792; DOI=10.1006/abio.1997.2558; Wilcken-Bergmann B., Schmidt M., Sobek H.,
                                                                                                                                                                                                                                                                                                                                                                                                                             BETA_LACTAMASE_A;
                                                                                                                                                                                                                                                                                                                                                                                                       Signal.
23
                                                                                                                                  213
                                                                                                                                                                                                                                                                                                                                                                                           31557 MW;
                                                                                                                                                                                                                                                                                                                                                    100.0%;
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EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                        Potential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for cloning of long polymerase lethal mutant of the crp gene
                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Extended-Spectrum Beta-Lactamases
                                                                                                                                                                                                                                                                                                                                                                                            5EB2F22753375FA9 CRC64;
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    (Fragment).
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Best Local S
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Query Match
Best Local Similarity
Matches 188; Conserv
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Topal M.D., Eadle J.S., Conrad M.;
"O-6-methylguanine mutation and repair is nonuniform:
DNA most interactive with O-6-methylguanine.";
J. Biol. Chem. 261:9879-9885(1986).
EMBL; M14017; AAA32208.1; -.
HSSP; Q9R435; 1HTZ.
Interpress 1 Traces 1 Trace
                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=U33;
Ghandili S., Hosseini-Mazinani
submitted (MAR-2004) to the EME
EMBL; AY583761; AAS86427.1; -.
HSSP; P00807; IALQ.
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Q6PRU7;
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                                                                                                                                   PROSITE; PS00146; BETA LACTAMASE_A;
NON TER 1 1 1
NON TER 232 232
SEQUENCE 232 AA; 25558 MW; 57910
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Inhibitor-resistant TEM beta-lactamase (Fragment).
                                                                                                                                                                                                                                                                          InterPro; IPR001466; Beta_lactamase. InterPro; IPR000871; Beta_lactamase_A. Pfam; PF00144; Beta-lactamase; 1. PRINTS; PR00118; BLACTAMASEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00146; BETA_LACTAMASE_A; 1.
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InterPro; IPR000871; Beta_lactamase_A.
Pfam; PF00144; Beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
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MEDLINE=86278026;
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Enterobacteriaceae; Escherichia.
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Viruses; ssDNA
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225 AA;
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nilarity 98.9%;
Conservative
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A viruses;
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                                99.5%; Score 970; DB 2; Length 232; 98.9%; Pred. No. 6.6e-74;
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EMBL/GenBank/DDBJ
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Pred. No. 6.4e-74;
1; Mismatches 1
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Best Local Simi
Matches 188;
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InterPro; IPRO01871; Beta_lactamase_A.
Pfam; PPO0144; Beta_lactamase; 1.
PRINTS; PRO0118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE_A; 1.
NON_TER 1.
NON_TER 255 255
SEQUENCE 255 AA; 27906 MW; DCBB28B65
Q84H49 PRELIMINARY;
Q84H49;
Q1-JUN-2003 (TrEMBLrel. 24, C
01-JUN-2003 (TrEMBLrel. 24, L
01-OCT-2003 (TrEMBLrel. 25, L
TEM-110 beta-lactamase (Fragm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q84H50;
Q84H50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-UN-2003 (TrEMBLrel. 24, Created)
01-UN-2003 (TrEMBLrel. 24, Last sequence update)
01-UCT-2003 (TrEMBLrel. 25, Last annotation updat
TEM-117 beta-lactamase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                             BOX A.T.A., Paauw A., Leverstein-vanHall M.A.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ
EMBL, AY130282; AAN05026.1; -.
HSSP; Q9R435; 1HTZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=562;
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                                                                                                                                 QLIDWMEADK
                                                                                                                                                                           KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ
                                                                                                                                                                                                            AGQBQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                                                                                                                       AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                 99.5%;
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                      Score 970; DB 2;
Pred. No. 7.4e-74;
1; Mismatches 1
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                                                           261
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             update)
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                                                                                                                                                                                                                                                                                                                            Length 255;
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                                                                Query Match
Best Local &
Matches 188
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Best Local
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ghandili S., Hosseini-Mazinani S.M.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AYS83762; AAS86428.1; --
HSSP; P00807; IALQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q6PRU6;
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
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Submitted (JUL-2002) to the
EMBL; AY130283; AAN05027.1;
HSSP; Q9R435; 1HTZ.
                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001466; Beta_lactamase.
InterPro; IPR000871; Beta_lactamase_A.
Pfam; PF00144; Beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Moraxellaceae; Acinetobacter.
NCBI_TaxID=269266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TEM beta-lactamase (Fragment).
Acinetobacter sp. Ull.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001466; Beta lactamase.
InterPro; IPR000871; Beta lactamase A.
Pfam; PF00144; Beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klebsiella oxytoca.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Klebsiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q6PRU6
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                                                                                                                                                                                                                                                                                                      PROSITE; PS00146; BETA_LACTAMASE_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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HPETLVKVKDAEDQLGARVGY1ELDLNSGK1LESFRPEERFPMMSTFKVLLCGAVLSRID
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                                                                                                                                                                                                 264
264 AA;
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261 AA;
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ilarity 98.9%;
Conservative
                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                               264
; 28986 MW;
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to the EMBL/GenBank/DDBJ
                                                             Score 970; DB Pred. No. 7.8e-
1; Mismatches
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Pred. No. 7.7e.
1; Mismatches
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                                                                                                                                                                                                         A4F071CF7489352C CRC64;
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                                                                                                DB 2; Length .8e-74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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RESULT 15
Q6QIVO
ID Q6QIVO
AC Q6QIVO
DT 05-JU
DT 105-JU
DT 
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-ES-42, ES-46, ES-71, and ES-11;
Yatsuyanagi J., Saito S., Harata S., Suzuki N., Amano K.
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY538700; AAS46846.1; -.
EMBL; AY538701; AAS46847.1; -.
EMBL; AY538702; AAS46848.1; -.
EMBL; AY538702; AAS46848.1; -.
EMBL; AY538702; AAS46848.1; -.
EMBL; AY538702; AAS46848.1; -.
EMBL; AY538702; AAS4684.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q6QIVO PRELIMINARY; PRT; 281 AA. Q6QIVO, 05-JUL-2004 (TrEMBLrel. 27, Created) 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) TEM-1 beta-lactamase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001466; Beta_lactamase. InterPro; IPR000871; Beta_lactamase_A. Pfam; PF00144; Beta-lactamase; 1. PRINTS; PR00118; BLACTAMASEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enterobacteriaceae; Serratia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Serratia marcescens.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=blaTEM-1;
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204
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281 AA;
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213
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Pred. No. 8.4e-74;
1; Mismatches 1
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Search completed: June 10, Job time : 63.6534 secs

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1: geneseqp1980s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ω	885	•	263	8	ADJ67709	
4	885	100.0	264	N	AAW16634	
Ŋ	885		264	N	AAW18680	_
σ	885	100.0	286	N	AAR31575	
7	885	•	286	N	AAR97619	_
8	885	٠	286	N	AAR96423	Aar96423 Cytochrom
9	885	100.0	286	N	AAW16635	Aaw16635 Beta-lact
10	885	100.0	286	N	AAW18679	Aaw18679 Secretory
11	885	100.0	286	N	AAY08529	Aay08529 Vector pA
12	885	100.0	286	w	AAB10442	Aab10442 Expressio
13	885	٠	286	w	AAB10438	-
14	885	•	286	ω	AAB10440	Aab10440 Expressio
15	885	100.0	286	4	AAB50898	
16	885	100.0	286	4	AAB31173	Aab31173 Amino aci
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18	885	•	286	6	ABP55474	
19	885	100.0	286	σ	ABR43622	Cloni
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21	885	100.0	286	8	ADR70410	Adr70410 Vector pA
22	885	100.0	286	œ	ADR70404	
23	885	100.0	286	8	ADR70416	Vector
24	885	100.0	286	œ	ADR70428	
25	885	100.0	290	4	AAU23219	5

13-JAN-2000; 2000US-0175968P. 15-MAR-2000; 2000US-00526106. 16-JAN-2001; 2001WO-US001651

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ALIGNMENTS

E. coli mature TEM-1 beta-lactamase.

24-SEP-2001 AAE05544;

(first entry)

AAE05544 standard;

protein;

263

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RESULT 1 AABO5544 ID AABO XX AABO XX Inte XX Inte XX Circ XX C Cleavage-site Region Cleavage-site Cleavage-site Interaction-dependent enzyme association; IdEA system; biosensor; circularly permutated interaction-activated protein; marker protein; type A beta-lactamase; TRM-1 beta-lactamase; protein-protein interaction; therapeutic; drug screening; thioredoxin; ampicillin resistance. Cleavage-site Cleavage-site Cleavage-site Region Escherichia coli. WO200151629-A2 Cleavage-site Active-site Cleavage-site Location/Qualifiers 27. .28 /note= "Break-point between alpha and 189. .204 _note= "Inter-sub-domain loop" 149. .150 note= "Break-point between alpha and 202. .203 /note= "Break-point between alpha and ?28. .229 190. .191 note= "Break-point between alpha and /note= "Inter-sub-domain loop" 38. .39 note= "Break-point between alpha and omega fragments" note= "Break-point between alpha and omega fragments" note= "Break-point between alpha note= "Break-point between alpha and omega fragments" . 40 .173 and omega omega omega omega omega fragments" fragments" fragments" fragments" fragments"

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                                                                                      RESULT 2
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CC The systems are also useful in selecting with a single marker protein the cc incorporation of multiple genetic traits in a host cell. In particular, the systems are useful in many applications in human therapeutics, co diagnostics and prognostics, as well as in high-throughput screening compositive and prognostics, as well as in high-throughput screening compositive and covery and validation of pharmaceutical targets and covery and validation of pharmaceutical targets and covery and validation of process two particular, yeast two particular, yeast two particular system or Selective Infective Phage System) require multiple steps of the discovery and the cause severe loss of efficiency compositive and false negative rates. The present system compositive and false negative rates. The present system compositive and false negative rates in the reaction of extra-cellular as well as intracellular proteins in a high throughput system compositive and false negative rates in a high throughput mapping of pair-wise protein composition and in continuous within and in continuous continuous system continuous within and in continuous continuous for any or signal transduction pathways, in high-continuous continuous system cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IdEA) systems that comprise a fusion sequence that encodes for a circularly permutated, interaction-activated proteins that reassemble to form functionally reconstituted marker proteins which produce a detectable signal upon the association of two oligopeptides, or upon simultaneous association of two oligopeptides with a third oligopeptide. The marker protein is preferably a type A beta-lactamase, especially TEM-1 beta-lactamase of Escherichia coli. The oligopeptide is a member of a proteome library selected from single chain antibody Fv fragment library, an antibody light chain variable region library and a peptide library displayed within thioredoxin. The IdEA systems are useful for detecting and identifying interactions between intracellular as well as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein-protein interaction. The present sequence is Escherichia coli mature TEM-1 beta-lactamase enzyme from plasmid pBR322. TEM-1 beta-lactamase is a product of ampicillin resistance gene. The enzyme has two domains, alpha-omega and mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interaction-dependent enzyme association systems for detecting interactions between two or three polypeptides, especially in human therapeutics, diagnostics or prognostics, comprise circularly permutated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Balint RF,
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                                AAB36692
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                                standard;
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ilarity 100.0%;
Conservative (
                             protein; 263
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Pred. No. 5.2e-90;
D; Mismatches 0;
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Best Local (
                                                                                                                                                                                                                                                                                                                                                        present invention are used for monitoring the occurrence of protein-
protein interactions in a sample, identifying oligopeptide interactions
between two different proteomes; identifying epitopes that bind to an
immunoglobulin (Ig) variable region, for identifying interactions between
an extracellular domain of a transmembrane protein and a polypeptide, for
high-throughput identification of compounds that inhibit phosphorylation-
regulated signal transducers, forming a enzyme complementation system for
selecting simultaneous incorporation of multiple genetic elements into a
host cell and for activating a beta-lactam derivative of an antitumour
compound in a host who is in need of it. The present sequence represents
the Escherichia coli mature TEM-1 beta-lactamase, which is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a fragment complementation system (I) which comprises a first oligopeptide (OP1) containing an N-terminal fragment with a C-terminal break point and a second oligopeptide (OP2) comprising a C-terminal with a N-terminal breakpoint, in which the C N terminal fragments are both derived from a marker protein (MP) and reassemble to form a functionally reconstituted MP. Methods from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel fragment complementation system to identify interactions between polypeptides comprises fragment pairs having first and second members that reassemble into a marker protein which has a directly detectable
                                                                                                                                                                                                                                                                                                                                      the Bscherichia coli mature TEM-1 beta-lactamase, exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Balint RF, Her J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAY-1999; 99US-0135926P.
13-JAN-2000; 2000US-0175968P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-MAR-2000; 2000WO-US007108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200071702-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interaction-activated protein; beta-lactamase; protein interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli mature TEM-1 beta-lactamase protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB36692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PANO-) PANORAMA RES INC.
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121
                                   121
                                                                                                                                                                                                                        al Similarity
172; Conserv
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                                                                                                                                                   \vdash
                     KELTAFLHMGDHVTRLDRWEPELNEAI PNDERDTTMPVAMATTLRKLLTGE 172
                                                                                            AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                                                                   HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERPPMMSTFKVLLCGAVLSRID
                                                                                                                                                                         HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                                                                        AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
KELTAFLHNMGDHVTRLDRWEPELNEAI PNDERDTTMPVAMATTLRKLLTGE
                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fig 2; 94pp; English.
                                                                                                                                                                                                                                                                                                     Ā
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                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                          Score 885; DB 4;
Pred. No. 5.2e-90;
; Mismatches 0;
                                                                                                                                                                                                                              Indels
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RESULT 3 ADJ67709

ADJ67709 standard; protein; 263

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The invention describes a fragment complementation system (I) comprising CC a first oligopeptide having an N-terminal fragment with a C-terminal CC break-point, and a second oligopeptide having a C-terminal fragment with CC a N-terminal break-point, where the N-terminal fragment and the CC terminal fragment each are derived from a marker protein and reassemble CC terminal fragment each are derived from a marker protein and reassemble CC terminal fragment each are derived from a marker protein and reassemble CC selecting simultaneous incorporation of multiple genetic elements into a CC compound in a host. The method described is useful for identifying a Second oligopeptide to which a first oligopeptide binds, involving coccapressing the first and second oligopeptides. Binding of the first CC oligopeptide to the second oligopeptides. Binding of the first CC oligopeptide to the second oligopeptides. Binding of the first CC oligopeptide to the second oligopeptides in the functional CC expressing the occurrence of protein-protein interactions in a sample; CC identifying oligopeptide interactions between two different proteemes; CC identifying epitopes that bind to an immunoglobulin variable region. CC (I) or an expression casette (II), encoding a selectable N or C-terminal CC peptide, is useful for identifying interactions between an extra cellular CC (II) is useful for high-throughput identification of compound that CC (II) is useful for high-throughput for protein, preferably CD40. (I) or an expression casette multiple interaction between extracellular and continued of a transmembrane protein with high throughput format. This is the amino acid contracellular protein with high throughput format. This is the amino acid contracellular protein with high throughput format.
sequence of antibiotic resistance enzyme TEM-1 beta-lactamase that used as a selectable gene in the fragment complementation system o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fragment complementation system for detecting immunoglobulin epitope, has first oligopeptide containing N-terminal fragment with C-terminal breakpoint, second oligopeptide containing C-terminal fragment with N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAY-1999;
13-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 beta-lactam derivative activation; anti-tumour compound; functional reassembly; protein-protein interaction; proteome interaction; immunoglobulin variable region; immune cell protein; CD40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 2; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-203222/19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-SEP-2003; 2003US-00668778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KALO-) KALOBIOS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ67708.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 99US-0124339P.
; 99US-0135926P.
; 2000US-0175968P.
; 2000US-00526106.
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antibiotic resistance;
    of the
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Sequence 263

Query Match Best Local Similarity Matches 172; Conserv

100.0%; (ilarity 100.0%;)
Conservative 0;

Score 885; DB 2; Pred. No. 5.2e-90; Mismatches 0;

Length 264;

Indels

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Gaps

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Sequence

264

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RESULT 4
ANAIL6634
ID MAN1634
ID MAN16634
ID MAN1634
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Best Local Similarity
Matches 172; Conserv
                                                                                Escherichia coli beta-lactamase (AAW16634), including the signal peptide, is the expression product of a molecular chimaera, designated pCMV-BL (AAT66737), in which the beta-lactamase gene is under control of the CMV intermediate/early promoter. Vectors consisting of a transcriptional regulatory DNA sequence linked to a beta-lactamase gene can be used for enzyme prodrug therapy. Expression of the beta-lactamase in a targetted cell allows conversion of a prodrug into an agent toxic to the cell for treatment of cancer, viral (e.g. HIV) infection or inflammation.

Secretion of the enzyme has the advantage of increasing neighbouring cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecular chimaera for gene or virus directed enzyme prodrug therapy useful for treatment of cancer, viral infection or inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAT66736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene directed enzyme prodrug therapy; GDEPT; virus directed enzyme prodrug therapy; VDEPT; beta-lactamase; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW16634 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HPETLVKVKDAEDQLGARVGY1ELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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                                                                                                                                                                                                                                                                                                                                                                                              28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .23
/label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                           38pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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Pred. No. 5.2e-
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                                                                                                          Matches
                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                            DNA construct for gene-directed enzyme prodrug therapy of lung cancer comprises lung- or neuroendocrine-specific promoter controlling expression of prodrug-converting enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prodrug therapy; gene directed enzyme virus directed enzyme prodrug therapy; beta-lactamase; pCMV-delBL.
                                                                                                                                                                                               lactamase constructs, placed under control of promoter/enhancer elements of lung-associated protein or neuroendocrine marker protein genes, can bused in novel chimaeric molecules for use in prodrug therapy of lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW18680 standard; protein; 264
                                                                                                                                                                                                                                     pCMV-delBL (AAT70311) in which a PCR-amplified beta-lactamase coding sequence, minus the signal sequence, is placed under control of the intermediate/early promoter of cytomegalovirus. Intracellular beta-
                                                                                                                                                                                                                                                                                                       Example 8iii; Page 32-34; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Intracellularly-expressed beta-lactamase.
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                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                         Dev I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-NOV-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-NOV-1996;
                                                                                                                                                                                                                                                                              intracellular form (AAW18680) of TEM beta-lactamase is expressed
                                                                                                                                                                                                                                                                                                                                                                                                 1997-298118/27.
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                                                                                                          172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                                                                    HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                                                                                                                                                             264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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                                                      HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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    AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                          Conservative
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                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                           PB
                                                                                                         0
                                                                                                       Score 885; DB 2;
Pred. No. 5.2e-90;
); Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prodrug therapy; GDEPT;
; VDEPT; lung cancer;
                                                                                                                                 Length
                                                                                                          Indels
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                                                                                                       Gaps
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121

KELTAFLHNMGDHVTRLDRWEPELNEAI PNDERDTTMPVAMATTLRKLLTGE

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RESULT 6
AAR31575
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                                                                                                                                 Query Match
Best Local
                                                                                                                   Matches 172;
                                                                                                                                                                                                                 The expression constructs pRNH127 and pRNH155 contain identical sequences but were constructed using different strategies (see AAQ36498). The constructs comprise exons 2-7 of human CYP1A1 gene under the construct of the inducible mouse metallothionein (MMT-1) promoter. The constructs also contain an open reading frame in the opposite orientation to the cytochrome P450 exons. This ORF encodes ampicillin resistance. The constructs are suitable for transformation of human fibroblasts derived from the xeroderma pigmentosum group A. Cultures of the transformed fibroblasts can be used to test substances for mutagenicity. The presence of the inducible cytochrome P450 gene allows metabolism of the substance to mutagenic metabolites. (Updated on 10-MAR-2003 to add missing OS
                                                                                                                                                                            Sequence 286
                                                                                                                                                                                                                                                                                                                                                                                                                                         In vitro method for testing mutagenicity of a chemical - by met-
chemical cell line consisting of transformed fibroblasts having
detectable cytochrome P450 mixed function oxidase activity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR31575
                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Col 21-24; 24pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                               gene damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  States JC, Hines RN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-JUN-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYPIA1; pRNH127; pRNH155; xeroderma pigmentosum group A; xenobiotics; circular; chimeric cytochrome P450IA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ampicillin resistance protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1993-052845/06.
DB; AAQ36498.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
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 84
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                                                                                      \vdash
                                                                                                                                  Similarity
                     AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGE 172
                                                          HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                                                                         HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; protein;
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 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                   Conservative
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                                                                                                                               100.0%;
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                                                                                                                   <u>,</u>
                                                                                                                 Score 885; DB 2;
Pred. No. 5.8e-90;
; Mismatches 0;
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                                                                                                                                             Length 286;
                                                                                                                    Indels
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RESULT 7
AAR97619
ID AAR9
AX AAR9
AX AAR9
AX Secx
XX Gene
KW Cytc
CK WO96
A 80
CCC A 80
CCC Cep
CCC Ce
RESULT 8
AAR96423
ID AAR9
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A secretory beta-lactamase (AAR97619) is expressed from DNA construct pCMV-BL (AAR99220), in which the beta-lactamase coding sequence is under the control of the intermediate/early cytomegalovirus promoter. Beta-lactamase delivery to mammalian cells confers sensitivity to cephalosporin prodrugs. Liposomal DNA/5-fluorouracil prodrug combinations resulted in s.c. tumour regression in mice bearing A549 tumours. Survival of mice bearing human large cell lung H460 intrathoracic (i.t.) tumours increased upon i.t. injection of the secretory beta-lactamase DNA was the secretory beta-lactamase DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecular chimaera for use in enzyme gene therapy - is activated in a target cell to express a secretable enzyme which cleaves a prodrug outside the cell into a cytotoxic or cytostatic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene therapy; gene directed enzyme prodrug therapy; GDEPT; virus directed enzyme prodrug therapy; VDEPT; prodrug activation; cytotoxic; cytostatic; cancer; tumour; retrovirus; vector;
AAR96423 standard; protein; 286 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 286
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N-PSDB; AAT29220.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                                                                                                                                                                                                                                                                                                                    AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                                                                                                                                                                                                                                                                                                                         HPETLVKVKDAEDQLGARVGY1ELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                                                                                                                                                                                         KELTAFLHNMGDHVTRLDRWEPELNEAI PNDERDTTMPVAMATTLRKLLTGE 172
                                                                                                                                                                                                                                                                                AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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                                                                                                                                                        KELTAFLHNMGDHVTRLDRWEPELNEAI PNDERDTTMPVAMATTLRKLLTGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 885; DB 2; llarity 100.0%; Pred. No. 5.8e-90; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 286;
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                                                                                                                                                     195
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RESULT 9
AAW16635
ID AAW1
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AAW16635

standard; protein;

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Query Match
Best Local S
Matches 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oxidase enyzmes expressed by the cells. Gene damage in the test cells is detected as an indication of cytotoxicity of the chemical. (Updated on 2: -MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Testing chemicals for cytotoxicity to human by using recombinant fibroblasts transformed with control of inducible promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hines RN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-JUN-1991;
09-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US5525482-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytochrome; P450; metallothionein; mouse; human; cytotoxicity; assay; metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytochrome P450 (CYPIA1 construct).
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25-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-NOV-1994;
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                                                 121
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                           KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGE 172
                                                                                                                                     AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                                                                                                                                HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                                                                                                                                                                                                                                                    HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
KELTAFLHNMGDHVTRLDRWEPELNEAI PNDERDTTMPVAMATTLRKLLTGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novak RF,
                                                                                                                                                                                                                                                                                                                      Conservative
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(first entry)
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92US-00990295.
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                                                                                                                                                                                                                                                                                                                   100.0%; Score 885; DB 2;
100.0%; Pred. No. 5.8e-90;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    detecting gene damage -
cytochrome P450 gene un
                                                                                                                                                                                                                                                                                                                                                                     Length 286;
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RESULT 10
AAW18679
ID AAW18
XX AAW18
AC AAW18
XX IS-AU
DT 13-AU
DX Secre
XX YITHS
KW Prodr
KW Virus
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                           is the expression product of a molecular chimaera, designated pcWV-delBL (AAT66738), in which the beta-lactamase gene is under control of the CMV intermediate/early promoter. Vectors consisting of a transcriptional regulatory DNA sequence linked to a beta-lactamase gene can be used for enzyme prodrug therapy. Intracellular expression of the beta-lactamase in a targetted cell allows conversion of a prodrug into an agent toxic to the cell for treatment of cancer, viral (e.g. HIV) infection or
Prodrug therapy; gene directed virus directed enzyme prodrug
                                         Secretory beta-lactamase.
                                                                 13-AUG-1997
                                                                                                                     AAW18679
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 286 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecular chimaera for gene or virus directed enzyme prodrug therapy useful for treatment of cancer, viral infection or inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-298117/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-NOV-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene directed enzyme prodrug therapy; ovirus directed enzyme prodrug therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beta-lactamase (no signal peptide).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                     inflammation
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                                                                                                                                                                                    144
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                                                                                                                                                                                                                                                                                                                                         172;
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                                                                                                                     standard; protein;
                                                                                                                                                                                                 KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGE 172
                                                                                                                                                                                                                                                                                                     HPETLVKVKDAEDQLGARVGY1ELDLNSGKILESFRPBERFPMMSTFKVLLCGAVLSRID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page
                                                                                                                                                                                                                                    AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                                                                                                                                                   AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                                                                                                                                                                                                     HPETLYKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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                                                                (first entry
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  directed enzyme prodrug therapy; GDEPT;
prodrug therapy; VDEPT; lung cancer;
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                                                                                                                                                                                                                                                                                                                                                    Score 885; DB 2;
Pred. No. 5.8e-90;
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RESULT 11
AAY08529
ID AAY08
XX AAY08
XX AAY08
XX AAY08
XX O3-AU
XX Vecto
XX Vecto
XX Firef
KW Firef
KW insec
XX insec
XX A
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Best Local
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N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                  The secreted form (AAW18679) of TEM beta-lactamase is expressed by pCMV-BL (AAT70309) in which a PCR-amplified beta-lactamase coding sequence is placed under control of the intermediate/early promoter of cytomegalovirus. Secretory beta-lactamase constructs, placed under control of promoter/enhancer elements of lung- associated protein or neuroendocrine marker protein genes, can be used in novel chimaeric molecules for use in prodrug therapy of lung cancer
                       Firefly; luciferase; tetracycline; transcriptional control; TetR; tetracycline repressor; tetracycline promoter; luminescence; luxCI insect; Tn10; medicine; dosage; cheese production; antibiotic; foc
                                                                         Vector pASK75 beta-la protein.
                                                                                                03-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 286 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 8ii; Page 26-27; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA construct for gene-directed enzyme prodrug therapy of lung comprises lung- or neuroendocrine-specific promoter controlling expression of prodrug-converting enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dev I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-NOV-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   beta-lactamase;
                                                                                                                         AAY08529
                                                                                                                                                  AAY08529 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1997-298118/27.
DB; AAT70309.
                                                                                                                                                                                                             144
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                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                             KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGE
                                                                                                                                                                                                                                                                                                             HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                                                                                                                                                                                                                                                                                   AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                                                                                                                                                                                                                                                     HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .23
/label=_Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24. .286
/label= Mat_protein
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                                                                                                                                                protein;
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                                                                                                  entry)
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                                                                                                                                                                                                                                                                                                                                                                         Score 885; DB 2;
Pred. No. 5.8e-90;
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                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                        286;
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                                                                                                                                                                                                                                       172
                           foodstuff;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer
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RESULT 12
AAB10442
ID AAB10
XX
AC AAB10
XX
AC AAB10
XX
XX
DT 01-DE
XX
XX
DE Expre
XX
KW Expre
KW B lym
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel tetracycline assay that uses recombinant CC prokaryotic cells comprising a luciferase gene under the transcriptional CC control of a tetracycline repressor and tetracycline promoter and CC involves the detection of luminescence emitted form the cells. The assay CC can be used to distinguish tetracycline form other microbial agents. The CC can be used to distinguish tetracycline form other microbial agents. The CC can be used to distinguish tetracycline form other microbial agents. The CC can be used to distinguish tetracycline form other microbial agents. The CC can be used to the insect luciferase gene, a tetracycline promoter (TetA) from Tnlo. The tetracycline promoter (TetA) from Tnlo. The tetracycline assay CC method can be used for the determination of tetracycline in a sample, CC e.g. to study the dosage and penetration of the medicine. The method can also be used to test cheese production, as cheese making bacteria are not able to work in the presence of tetracycline. The method can also be used to determine the presence of tetracycline. The method can also be used for the discrobes as do conventional tests, and so is much more rapid. CC e.g. for allergic people. The present assay method does not rely on the growth of microbes as do conventional tests, and so is much more rapid. CC luminescence can be detected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 286 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-338015/28
N-PSDB; AAV72418.
                                                                                                                               AAB10442
                                                                                                                                                                AAB10442 standard; protein; 286 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KORP/)
(KARP/)
(KURI/)
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                                                      Expression vector pSEX15G2 bla protein.
                                                                                                                                                                                                                                                            144
                                                                                                                                                                                                                                                                                               121
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                                                                                                                                                                                                                                                                                                                                                         61 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
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) KARP M.
) KURITTU J.
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                                                                                                                                                                                                                                                                                                                                                                                                           HPETLVKVKDAEDQLGARVGY1ELDLNSGK1LBSFRPEERFPMMSTFKVLLCGAVLSR1D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for tetracycline using recombinant prokaryotic cells
                                                                                                                                                                                                                                                                                     KELTAFLHNMGDHVTRLDRWEPELNBAIPNDERDTTMPVAMATTLRKLLTGE 172
                                                                                                                                                                                                                                                                                                                                    AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                                                                                                                                                            KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGE 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 885; DB 2; Length 286; Pred. No. 5.8e-90; Indels
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                                                                                                                                                                                                                                                                                                                                     143
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Expression vector; antibody binding protein; monoclonal antibody; Neo-R; B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.

Expression vector; antibody binding protein; monoclonal antibody; Neo-R;

Expression vector pSEX11L4 bla protein

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RESULT 13
AAB10438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC This invention describes a novel method for the selection of monoclonal CC antibodies (MAD) which comprises (i) fusing B lymphocytes with myeloma CC cells to produce antibody-producing hybridomas such that the antibodies CC are presented at the surface of the hybridomas by an antibody-binding CC protein (I); and (ii) binding the antibody to antigens (Ag). The CC invention also describes antibody-binding proteins (I) that comprise a CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa CC chain or a murine MFC (major histocompatibility complex) Class I k(k) CC molecule; an antibody-binding site of proteins A, G, L or LG, and the CC transmembrane domain of PDGFR (platelet-derived growth factor receptor) CC or CD52. The method is used to select MAD with specificity for particular CC antigens. MAD can be selected without separate culture of hybridomas, and CC election can be made against many antigens in a library, optionally on the basis of strength of affinity for a particular antigen. Complex CC mixtures of hybridomas can be used for selection, reducing the time and CC mixtures of hybridomas can be used for selection, reducing the time and CC mixtures of hybridomas can be used for selection, reducing the time and CC motein contained in the expression vector pSEXI5G2 which contains the CC bla protein, Neo-R and protein G described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Simi
Matches 172;
                                                                                                          AAB10438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 286
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                                                                       01-DEC-2000
                                                                                                                                              AAB10438 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Selecting monoclonal antibodies, by expressing them on the surface hybridomas attached to antibody-binding protein, then reaction with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 885; DB 3;
100.0%; Pred. No. 5.8e-90;
htive 0; Mismatches 0;
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                               Expression vector pSEX11G2 bla protein
                                                                  01-DEC-2000
                                                                                                   AAB10440;
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                                                                                                                                     AAB10440 standard; protein; 286
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172; Conserv
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                                                                                                                                                                                                                                                                                                  AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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                                                                                                                                                                                                                                                                                                                                                                      HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 83
                                                                                                                                                                                                                             KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGE 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; ilarity 100.0%; Conservative 0
                                                                  (first entry)
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Pred. No. 5.8e-90;
D; Mismatches 0;
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel method for the selection of monoclonal calls to produce antibody-producing hybridomas such that the antibodies cells to produce antibody-producing hybridomas such that the antibodies care presented at the surface of the hybridomas by an antibody-binding compression (I); and (ii) binding the antibody to antigens (Ag). The combination of the signal peptide of a murine immunoglobulin (Ig) kappa combination or a murine MHC (major histocompatibility complex) Class I k(k) conclude; an antibody-binding site of proteins A, G, L or LG, and the cultivate domain of protein of proteins A, G, L or LG, and the cultivate domain of protein contained antigens which specificity for particular cross-control be made against many antigens in a library, optionally on the basis of strength of affinity for a particular antigen. Complex cost involved in Mab selection. This sequence represents the bla protein contained in the expression vector pSEXIIG2 which contains the invention of the basis of strength of affinity for a particular antigen the bla protein contained in the expression vector pSEXIIG2 which contains the contains the protein of the invention to the contains the protein of the invention to the contains the protein contains the protein of described in the method of the invention to the contains the protein contains the protein of described in the method of the invention to the contains the protein contains the protein of described in the method of the invention to the contains the protein of the invention to the contains the protein of described in the method of the invention to the contains the protein of the invention to the contains the protein of described in the method of the invention to the contains the protein of the invention to the protein of the invention to the contains the protein of the protein of described in the method of the invention to the protein of the 
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 286 AA;
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                                         20-MAR-2001
                                                                                       AAB50898
                                                                                                                                   AAB50898 standard; protein; 286
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                                                                                                                                                                                                                                                                                                                                               AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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Pred. No. 5.8e-90;
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Protein encoded by bla resistance marker

of integration vector pLO12306

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Best Local S
Matches 172
                                                                                                                                                                                                                                                                                                                                                 control of a surrogate promoter capable of increasing expression of the polysaccharase. The host cell also contains a second heterologous polynucleotide encoding a secretory polypeptide to facilitate the secretion of the expressed polysaccharase. The recombinant host cell is useful for producing polysaccharase which is useful for enzymatically degrading oligosaccharides such as lignocellulose, hemicellulose, cellulose, pectin or their combinations, and fermenting the product to ethanol, by simultaneous saccharification and fermentation processes. The present sequence is encoded by an integration vector which was introduced into cells to generate recombinant host cells. The vector contains a surrogate promoter from Zymomonas mobilis, the celZ gene from Erwinia chrysanthemi, resistance markers bla and tet, and Klebsiella oxytoca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bla resistance marker; recombinant host cell; saccharification; fermentation; polysaccharase; oligosaccharide degradation; celZ gene; glucanase; integration vector; pLO12306.
                                                                                                                                                                                                                                                                                                  Sequence 286 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is given in a specification relating to a recombinant host cell suitable for simultaneous saccharification and fermentation. The host cell contains at least one heterologous polynucleotide encoding a polysaccharase under the transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant host cells useful for producing polysaccharase for degrading oligosaccharides, comprises a first heterologous polynucleotide encoding polysaccharase under control of surrogate promoter.
                                                                                                                                                                                                                                                                                                                                        target sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 82-83; 87pp; English.
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144
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                                                                                                                                               AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGF 120
                     KELTAFLHNMGDHVTRLDRWEPELNBAIPNDERDTTMPVAMATTLRKLLTGE 172
                                                                        AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 143
KELTAPLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGE 195
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Search completed: June 10, 2005, 10:49:12 Job time : 67.6888 secs

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Result
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Listing first 45 summaries
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2: uniprot_trembl:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Q79016
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Q84H49
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Q84H49
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Q6PRU7
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RESULT 2
Q6WWY4
ID Q6WW
AC Q6WW
DT 05-J
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GGWWY4 PRELIMINARY; PRT; 232 AA.
GGWWY4;
05-WUL-2004 (TYEMBLrel. 27, Created)
05-WUL-2004 (TYEMBLrel. 27, Last sequence update)
05-WUL-2004 (TYEMBLrel. 27, Last annotation update)
Beta-lactamase (Fragment).
Name=blaTEM;
Hafnia alvei.

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Obert C.A., Goldstone C.M., Go
Submitted (APR-2004) to the ER
EMBL; AY265882; AAP93840.1; -
HSSP; P00807; IKGE.
HSSP; P00807; IKGE.
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SEQUENCE
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
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Submitted (APR-2004) to the
EMBL; AY265886; AAP93844.1;
HSSP; P00807; 1KGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001466; Beta lactamase.
InterPro; IPR000871; Beta lactamase A.
Pfam; PF00144; Beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Klebsiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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PRINTS; PI
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Enterobacteriaceae; Hafnia
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00146; BETA_LACTAMASE_A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=blaTEM;
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                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                  149;
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PR00118; BLACTAMASEA.
                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                  HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEBRFPMMSTFKVLLCGAVLSRID
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                                  AGOEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                   HPETLVKVKDAEDQLGARVGY1ELDLNSGK1LESFRPEERFPMMSTFKVLLCGAVLSR1D
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241
241 AA;
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232 AA;
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                                                                                                                                                                                                                                                                                                                                                                 241
26407 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gordon D.M., Riley EMBL/GenBank/DDBJ c
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Pred. No. 1.7e-62;
; Mismatches 0;
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databases.
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databases.
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Best Local S
Matches 149
SEQUENCE FROM N.A.
TISSUB=First leaf;
Jansen C., Korell M., Eckey C
Submitted (MAY-2004) to the E
EMBL; AJ717739; CAG30723.1; -
HSSP; P00807; IALQ.
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                                                                                                                                                                                                                   Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; E
Spermatophyta; Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation updat
Hypothetical protein (Fragment).
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InterPro; IPR000871; Beta_lactamase_A.
Pfam; PF00144; Beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE_A; 1.
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                                                                                                                                                                      NCBI_TaxID=4513;
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Enterobacteriaceae; Eschei
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                                                  C., Biedenkopf D.,
EMBL/GenBank/DDBJ 
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EMBL/GenBank/DDBJ databa
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                                                                                                                                                                                                                           Embryophyta; Tracheophyta;
a; Poales; Poaceae; Pooidea
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Best Local S
Matches 149
                                                                                                                                                                                                                                                                                                                                                                                          Henrich B., Schmidtberger B.;

"A variant of phix174 gene B-based positive selection vector enhanced lytic potential.";

Gene 154.51-54(1995).

R EMBL; Z35638; CAA84692.1; -.

R PIR; S47061; S47061.

R HSSP; Q97435; 1HTZ.

R InterPro; IPR001466; Beta lactamase.

R InterPro; IPR000871; Beta_lactamase_A.

R InterPro; IPR000871; Beta_lactamase_A.

R PRINTS; PR00114; Beta_lactamase; 1.

R PFINTS; PR00118; BACTAMASEA; 1.

SEQUENCE 286 AA; 31557 MW; SEB2F22753375FA9 CRC64;
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Best Local
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Q38058; PRELIMINARY;
Q18058;
Q1-NOV-1996 (TrEMBLrel. 01,
Q1-NOV-1996 (TrEMBLrel. 24,
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PROSITE; PS00146; BETA_LACTAWASE_A;
Hypothetical protein.
NON_TER 285 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=95172401; PubMed=7867948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteriophage phi-X174. Viruses; ssDNA viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=bla;
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Pfam; PF00144; Beta-lactamase; 1.
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InterPro; IPR000871; Beta_lactamase_A.
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                            KELTAFLHNMGDHVTRLDRWEPELNEAIP 149
                                                                                                AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                               AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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                                                                                                                                                                                                                                                                                                    Conservative
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annotation
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RESULT

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RESULT
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Best Local S
Matches 149
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C PLASMID=J3356/pox7/1;

C PLASMID=J3356/pox7/3, and J3356/POX7/1;

X MEDLINE=96422755; PubMede8825372; DOI=10.1006/plas.1995.0005;

X Meedham C., Noble W.C., Dyke K.G.;

"The stabhylococcal insertion sequence IS257 is active.";

I Plasmid 34:198-205(1995).

R EMBL; U36912; AAB39957.1; -.

R EMBL; U36912; AAB39957.1; -.

R InterPro; IPR00146; Beta lactamase.

InterPro; IPR00146; Beta lactamase A.

PINTTS; PR00114; Beta-lactamase; 1.

R Pfam; PF00144; Beta-lactamase; 1.

R PFAM; PR00116; BEACTAMASEA.

R PROSITE; PS00146; BETA_LACTAMASE A; 1.
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Q79CL6;
05-JUL-2004
05-JUL-2004
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Q00626; O08022; O08102; O09393; O09396; O09397; O09398;
Q09400; O09401; O09402; O09403; O09404; O09405; O09406;
Q09408; O09481; O09482; O09490; Q57339;
Q1-NOV-1996 (TERMELTE1. 01, Created)
Q1-NOV-1996 (TERMELTE1. 01, Last sequence update)
Q5-OCT-2004 (TERMELTE1. 28, Last annotation update)
                                                                                                                            SEQUENCE FROM N.A.

MEDLINE=97074643; PubMed=8917070; DOI=10.1016/0378-1119(96)00114-X;
Serebrijski I.G., Vassin V.M., Tsygankov Y.D.;

"Two new members of the BioB superfamily: cloning, sequencing and expression of bioB genes of Methylobacillus flagellatum and Corynebacterium glutamicum.";

Gene 175:15-22(1996).
SEQUENCE FROM N.A.
Serebrijski I., Vassin V., 7
Submitted (JUL-1995) to the
EMBL; U31280; AAC44581.1; -.
                                                                                                                                                                                                                                                                                                                                                            Methylobacillus flagellatum.
Bacteria; Proteobacteria; Betaproteobacteria;
Methylophilaceae; Methylobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid J3356/pOX7/3, Bacteria; Firmicutes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286 AA;
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(TrEMBLrel. 27, Last seq
(TrEMBLrel. 27, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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Bacillales;
                          Tsygankov Y.;

EMBL/GenBank/DDBJ
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Pred. No. 2.2e-62;
; Mismatches 0;
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Q79DR3
                                                    Jeong S.H., Bae I.K., Lee J.H., Sohn S.G., Kang G Kim Y.H., Jeong B.C., Lee S.H.;
"Molecular Characterization of Extended-Spectrum produced by Clinical Isolates of Klebsiella pneum coli from a Korean Nationwide Survey.";
J. Clin. Microbiol. 42:2902-2906(2004).
EMBL; M74750; AAA24057.1;
EMBL; Y12694; CAA73226.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001466; Beta_lactamase.
InterPro; IPR000871; Beta_lactamase_A.
Pfam; PF00144; Beta_lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE A; 1.
PROSITE; PS00146; BETA_LACTAMASE A; 1.
SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9
                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98189310;
Schlieper D., Von
Mueller-Hill B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=K12; PLASMID=pRP4;
Rondot S., Anthony K., Dul
Little M., Breitling F.;
Submitted (APR-1997) to t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maneewannakul K., Maneewannakul S., Ippen-Ihler K.; Submitted (AUG-1991) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=K-12;
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Escherichia coli.",
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria;
                                                                                                                                                                                                                                      PubMed=15243036;
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               AJ001614; CAA04868.1;
AY425988; AAQ95605.1;
                                                                                                                                                                                                                                                                                                      Biochem.
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Wilcken-Bergmann
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Last annotation update)
ta-lactamase precursor (
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Pred. No. 2.2e-62;
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n B., Schmidt M., Sobek H.,
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Q38212;
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GO; GO:0008800; F:beta-lactamase activity;
GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR001466; Beta_lactamase.
InterPro; IPR001871; Beta_lactamase_A.
Pfam; PF001144; Beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE_A; 1.
                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=86278026; PubMed=3525535;
Topal M.D., Eadie J.S., Conrad M.;
Topal M.D., Eadie J.S., Conrad M.;
"O-6-methylguanine mutation and repair is nonuniform:
DNA most interactive with O-6-methylguanine.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Bacteriophage f1-R208 ampicillinase gene mutation.
Bacteriophage f1.
Viruses; ssDNA viruses; Inoviridae; Inovirus.
                                                                                                                                                                                                                                                                                      EMBL; M14017; AAA32208.1; -.
HSSP; Q9R435; 1HTZ.
InterPro; IPR001466; Beta_lactamase.
InterPro; IPR000871; Beta_lactamase_A.
Pfam; PF00144; Beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
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PROSITE; PS00146; BETA LACTAMASE_A;
NON TER 1 1 009BE
SEQUENCE 225 AA; 25022 MW; 009BE
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SIGNAL 1 23
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                                                                                                                                                                              Score 769; DB 2;
Pred. No. 2.1e-62;
1; Mismatches 0
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Pred. No. 2.2e-62;
Mismatches 0;
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ID PRUT
OF
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Q84150
ID Q8415
AC Q8445
DT 01-U
DT 01-U
DT 01-O
DB TEM-I
OC Bacte
OC Bacte
OC CATE
OC NCBI
RA BOX A
RA BOX A
RA BOX A
RI SUDMI
DR HSSP;
DR Intex
DR Intex
DR PRIMI
DR PRIMI
DR PRIMI
DR PRIMI
DR PRIMI
DR FARN
DR FRIMI
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DR FRIMI
DR SCOULT
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Best Local (
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01-JUN-2003 (TrEMBLrel. 24, Created
01-JUN-2003 (TrEMBLrel. 24, Last se
01-OCT-2003 (TrEMBLrel. 25, Last ar
TEM-117 beta-lactamase (Fragment).
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SEQUENCE
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BOX A.T.A., Paauw A., Leverstein-vanHall M.A.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ EMBL; AY130382; AAN05026.1; -.

HSSP; Q9R435; 1HTZ.
                                 NON_TER
                                                                                      InterPro; IPR001466; Beta_lactamase.
InterPro; IPR000871; Beta_lactamase_A.
Pfam; PF00144; Beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE_A; 1.
NON, TETE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001466; Beta_lactamase.
InterPro; IPR000871; Beta_lactamase_A.
Pfam; PF00144; Beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
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Submitted (MAR-2004) to the EMBL/Geni
EMBL; AY583761; AAS86427.1; --
HSSP; P00807; IALQ.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Inhibitor resistant TEM beta-lactamase (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q84H50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q6PRU7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRVD
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232 AA;
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1: 25558 MW;
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27906
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                                                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ databases
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   DCBB28B65978C3A6
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RESULT 14
QGERUG
ID QGERU
AC QGERU
AC QGERU
DT 05-JU
DT 05-JU
DT 05-JU
DT 05-JU
DT TEM b
OS Acine
OC Bacte
OC MORAX
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ID Q8444
AC Q8444
AC Q8444
AC Q8464
DT 01-JU
DT 01-JU
DT 01-GC
DB TEM-1
OS Klebs
OC Enter
OX NCBI
RP SEQUE
RA BOX A
RL Submil
DR EMBL;
DR HSSP;
DR Intex
DR Intex
DR Intex
DR FINT
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DR PROSI

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Best Local
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Q6PRU6;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
TEM beta-lactamase (Fragment).
Acinetobacter sp. Ull.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Acinetobacter.
NCBI_TaxID=269266;
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Q84H49;
01-JUN-2003
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Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Klebsiella.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat-
TEM-110 beta-lactamase (Fragment).
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NON TER 1 1
NON TER 261 261
SEQUENCE 261 AA; 28738 MW; 4F740
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                                                                                                                                                                                                                                           Q6PRU6
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                                                                                                                                                                                                                                                                                                                                                                                                                        KELTAFLHNMGDHVTRLDRWEPELNEAIP 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KELTAFLHNMGDHVTRLDRWEPELNEAIP 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
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28738 MW; 4F748F7733A08CBB CRC64;
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Pred. No. 2.4e-62;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 769; DB 2; Length 261; Pred. No. 2.5e-62; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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SEQUENCE FROM N.A.

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Q6QIVO AC Q6QIV AC Q6QIV DT 05-JU DT 05-JU DT 05-JU DT 05-JU DT 05-JU DT 15M-1
GN Name= OS Serra OS NCBI CO Bacte OC Bacte OC Bacte OC Bacte OC STRAI I DR SEQUE RO STRAI I L SUBMI DR EMBL; DR Inter DR Inter DR PRINT DR 
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Matches 148; Conserva
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SEQUENCE FROM N.A.
STRAIN=ES-42, ES-46, ES-71, and ES-11;
Yateuyanagi J., Saito S., Harata S., Suzuki N., Amano K.-I.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY538700; AAS46846.1; -.
EMBL; AY538701; AAS46847.1; -.
EMBL; AY538702; AAS46844.1; -.
EMBL; AY538702; AAS46844.1; -.
EMBL; AY538690; AAS46844.1; -.
EMBL; AY538670; IALQ.
InterPro; IPR001466; Beta lactamase.
InterPro; IPR001467; Beta—lactamase.
InterPro; IPR001871; Beta—lactamase.
InterPro; IPR001871; Beta—lactamase.
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SEQUENCE
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NON TER 281 281 SEQUENCE 281 AA; 30837 MW; C8934B9C696057BF CRC64;
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Ghandili S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS;
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S; PR00118; BLACTAMASEA.
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                                                                                                                           HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRVD 83
                                                                                                                                                                                HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60
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                                   AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
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                                                                                                                                                                                                                                                                                     99.9%; Score 769; DB 2; Length 281; ilarity 99.3%; Pred. No. 2.7e-62; Conservative 1; Mismatches 0; Indels
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; 28986 MW; A4F071CF7489352C CRC64;
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Search completed: June 10, 2005, Job time: 50.9177 secs 10:57:01

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KELTAFLHNMGDHVTRLDRWEPELNEAIP 172

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Title:
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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A60448

A60632

A44998

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305 2 A61152 305 2 A61166 305 2 A67002 305 2 A60680 314 1 PNSMIU 311 1 S02714 294 2 S16553 293 2 S04649 307 1 PNBSL 293 2 S42075 306 1 PNBSU 306 1 PNBSU 306 1 PNBSU 306 1 PNBSU 306 2 S42075 294 2 S44080 310 2 JL0091	293
2 A61156 2 A61166 2 A57002 2 A57002 2 A60680 1 PNSU1U 1 S02714 2 S16553 2 S04649 1 PNBSU 2 A54543 2 S42075 1 PNBSU 2 PNBSU 2 S03167 2 S44080 2 JL0091	38.1
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	N
beta-lactamase	JL0091

ALIGNMENTS

C;Species: Schizosaccharomyces pombe C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000 C;Accession: T51301

(EC 3.5.2.6) - fission yeast (Schizosaccharomyces pombe)

beta-lactamase

T51301

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R;Henrich, B.; Schmidtberger, B. submitted to the EMBL Data Library, A;Description: A variant of phiX174
                                                                                                                                                               beta-lactamase (BC 3.5.2.6) - phage phi
C;Species: phage phi-X174
C;Date: 13-Jan-1995 #sequence_revision
C;Accession: S47661
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-286 <HEN>
A;Cross-references: UNIPROT:Q38058; EMBL:Z35638; NID:g520996; PIDN:CAA84692.1; PID:g52099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-286 <WAC>
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Yeast 13, 1065-1075, 1997
A;Title: Heterologous HIS3 marker and G
A;Reference number: Z09587
                                                                            A; Reference number: S47060
A; Accession: S47061
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C;Superfamily: beta-lactamase
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C;Genetics:
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Similarity 100.0%;
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Pred. No. 1.9e-66;
); Mismatches 0;
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                                                                                                              July 1994
gene E-based
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                                                                                                                                                                                    13-Jan-1995 #text_change 09-Jul-2004
                                                                                                                positive selection vectors with
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C;Species: Escherichia coli
C;Date: 30-Nov-1980 #sequence revision 01-Sep-1981 #text_change
C;Accession: A93821; A93820; A35387; S24415; A01005
R;Sutcliffe, J.G.
Proc. Natl. Acad. Sci. U.S.A. 75, 3737-3741, 1978
A;Title: Nucleotide sequence of the ampicillin resistance gene o
A;Reference number: A93821; MUID:79012484; PMID:358200
A;Accession: A93821
A;Experimental source: plasmid pBR322 R;Ambler, R.P.; Scott, G.K. Proc. Natl. Acad. Sci. U.S.A. 75, 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X76682; NID:g453622; PIDN:CAA54104.1; PID:g453623
A;Note: submitted to the EMBL Data Library, December 1993
C;Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Universal beta-galactosidase cloning vectors for promoter A;Reference number: A57991; MUID:95011660; PMID:7926839 A;Accession: S41975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: S41975
R;Kaestner, K.H.; Montoliu, L.;
Gene 148, 67-70, 1994
                                                                              A; Molecule type: DNA
A; Residues: 1-286 < SUT>
                                                                                                                                                                                                                                                                              beta-lactamase (EC 3.5.2.6) precursor - Escherichia coli plasmids
N;Alternate names: beta-lactamase TEM-6 (for blaT-6 DNA); penicillinase
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A; Residues: 1-286 < KAE>
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;Keywords: hydrolase
                                                          ;Cross-references: UNIPROT:P00810; GB:V00613; GB:J01832; NID:G43710; PIDN:CAA23886.1;
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Date: 25-Dec-1994 #sequence_revision 22-Aug-1996 #text_change 20-Oct-2000;
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  3732-3736, 1978
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Pred. No. 1.9e-66;
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Pred. No. 1.9e-66;
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                    A; Molecule type: DNA
A: Residues: 1-286 < RES>
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  A;Residues: 1-286 <R
A;Cross-references:
                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
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beta-lactamase (EC 3.5.2.6) - synthetic
C:Species: synthetic
A;Note: cloning vector pCG1408 engineered and expressed in Clavibacter xyli subsp. cynode
C:Date: 15-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Oct-2000
C;Accession: I40905
C;Accession: I40905
C;RCession: J.; Stearman, R.S.; Uratani, B.B.
Plasmid 29, 21-24, 1993
A;Title: Development of a native plasmid as a cloning vector in Clavibacter xyli subsp. c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Keywords: antibiotic resistance; hydrolase; membrane protein F;1-23/Domain: signal sequence #status predicted <SIG>F;24-286/Product: beta-lactamase #status experimental <MAT>F;68/Active site: Ser #status predicted F;75-121/Disulfide bonds: #status predicted
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Cold Spring Harb. Symp. Quant. Biol. 43, 77-90, 1979

A;Title: Complete nucleotide sequence of the Escherichia

A;Reference number: A90923; MUID:80002802; PMID:383387

A;Contents: annotation
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A;Cross-references: EMBL:X57972; NID:g41816; PIDN:CAA41038.1; PID:g41817
A;Experimental source: ISI-11ke blaT-6 DNA
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A;Title: The kil-kor regulon of broad-host-range plasmid RK2: nucleotide sequence, A;Reference number: A35387; MUID:90264294; PMID:2160936
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R;Goussard, S.; Sougakoff, W.; Mabilat, C.; Bauernfeind, A.; Courvalin, P.
J. Gen. Microbiol. 137, 2681-2687, 1991
A;Title: An ISI-like element is responsible for high-level synthesis of extended-spectrum A;Reference number: S24415; MVID:92166702; PMID:1665171
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A;Residues: 24-36,'K',38-286 <AMB>
A;Rsperimental source: plasmid R6K
R;Kornacki, J.A.; Burlage, R.S.; F
A; Accession: I40905
                      A; Reference number: 140904;
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A;Residues: 182-286 <KOR>
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                         a native plasmid as
904; MUID:93361581; E
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Pred. No. 2.4e-66;
1; Mismatches 0
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EMBL: U21228; NID: 9885956; PIDN: AAA70411.1;

PID:g885958

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extended spectrum beta-lactamase CAZ-7 - Klebsiella pneumoniae C;Species: Klebsiella pneumoniae C;Species: Klebsiella pneumoniae C;Species: Klebsiella pneumoniae C;Date: 12-Appr-1996 #sequence_revision 19-Appr-1996 #text_change 22-Jun-1999 C;Accession: $60312 R;Chanal, C.; Sirot, M.C.; Sirot, D.; Labia, R.; Sirot, J.; Cluzel, R. Artimicrob. Agents Chemother: 36, 1817-1820, 1992 A;Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase gene A;Reference number: $60310; MUID:93037315; PMID:1416873 A;Accession: $60312 A;Scatus: preliminary; translation not shown A;Residues: 1-286 <CHA A;Residues: 1-286 <CHA A;Residues: 1-286 <CHA A;Residues: 1-286 <CHA A;Residues: beta-lactamase I
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C;Superfamily: beta-lactamase I
C;Keywords: antibiotic resistance; hydrolase
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A; Residues: 1-286 < MAB>
A; Cross-references: UNIPROT: P00810;
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A;Title: A new example of physical linkage between Tn1 and A;Reference number: S30112; MUID:93062798; PMID:1331747
A;Accession: S30113
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milarity 98.0%;
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Pred. No. 1.4e-65;
3; Mismatches 0;
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beta-lactamase (EC 3.5.2.6) TEM-1 - Klebsiella pneumoniae transposon Tn1331 C;Species: Klebsiella pneumoniae C;Species: Klebsiella pneumoniae C;Date: 12-Apr-1996 #sequence revision 19-Apr-1996 #text_change 09-Jul-2004 C;Accession: S60311; B37392; FQ0498 R;Chanal, C.; Poupart, M.C.; Sirot, D.; Labia, R.; Sirot, J.; Cluzel, R. Antimicrob. Agente Chemother. 36, 1817-1820, 1992 A;Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase gen. A;Reference number: S60310; MUID:93037315; PMID:1416873 A;Accession: S60311
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R;Chanal, C.; Poupart, M.C.; Sirot, D.; Labia, R.; Sirot, J.; Cluzel, R. Antimicrob. Agents Chemother. 36, 1817-1820, 1992
A;Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase gene A;Reference number: S60310; MUID:93037315; PMID:1416873
A;Accession: S60310
A;Title: Sequencing and expression of aadA, bla, and tnpR A;Reference number: A37392; MUID:91172904; PMID:1963948 A;Accession: F37392 A;Accession: F37392 A;Molecule type: DNA
                                                                                                                   A;Cross-references: UNIPROT:Q99224; EMBL:X65253; NID:g296953; PIDN:CAA46345.1; PID:g29695
R;Tolmasky, M.E.
Plasmid 24, 218-226, 1990
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A; Residues: 1-286 < CHA>
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Best Local Similarity
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97.3%;
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Pred. No. 5.2e-65;
3; Mismatches 1

    Mismatches

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beta-lactamase (EC 3.5.2.6) 2A precursor - Klebsiella pneumoniae plasmids N,Alternate names: beta-lactamase SHY2A C;Species: Klebsiella pneumoniae c;Species: Klebsiella pneumoniae C;Date: 21.Nov-1993 #sequence revision 10-Nov-1995 #text_change 15-Oct-1999 C;Accession: S16146; A35395; S18767 R;Podbielski, A.; Schoenling, J.; Melzer, B.; Warnatz, K.; Leusch, H.G. J. Gen. Microbiol. 137, 569-578, 1991 J. Gen. Microbiol. 137, 569-578, 1991 A;Title: Molecular characterization of a new plasmid-encoded SHV-type beta-lactamase A;Reference number: S16146; MUID:91237320; PMID:2033379 A;Accession: S16146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             r.asmid 27, 220-230, 1992
A;Title: Complete nucleotide sequence and gene organization of plasmid NTP16.
A;Reference number: JQ1538; MUID:92383313; PMID:1325061
A;Arcfession: JQ1546
A:Status.
                                                                                                                                                                                        RESULT
S16146
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C;Superfamily: beta-lactamase I
C;Keywords: antibiotic resistance; hydrolase
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A;Cross-references: GB:M55547; NID:g155010; PIDN:AAA98408.1; C;Genetics:
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C;Genetics:
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A; Residues: 1-286 < CAN>
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Best Local
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mily: beta-lactamase
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97.3%;
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Pred. No. 5.2e-65;
3; Mismatches 1
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Pred. No. 5.2e-65;
1; Mismatches 2;
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C;Superfamily: beta-lactamase I
C;Keywords: antibiotic resistan
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A; Residues: 1-286
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A; Residues: 1-286 <GAR>
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Best Local Similarity 70.39
Conservative
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                                                                                                                                                                                                                                                                                                             Superfamily: Beta-lactamase I Keywords: antibiotic resistant
                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                             21/Domain:
                     143
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                                                                                                                                                                                                                                             Similarity
                                     ELTAFLHNMGDHVTRLDRWEPELNEAIP 149
                     GLTAFLRQIGDNVTRLDRWETELNEALP
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                                                                                                                                                                                                                                                                                             sequence #status
                                                                                                                                                                                                                                                                                                                 resistance; hydrolase
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A;Molecule type: DNA
A;Residues: 1-30,'L',32-286 <LEE>
A;Cross-references: GB:X62115; NID:948988; PIDN:CAA44025.1;
A;Experimental source: plasmid BWH77
C;Genetics:
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R,Lee, K.Y.; Hopkins, J.D.; Syvanen, M.
J. Bacteriol. 172, 3229-3236, 1990
A,Title: Direct involvement of IS26 in an antibiotic resistance A,Reference number: A35395; MUID:90264317; PMID:2160941
A,Accession: A35395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Garbarg-Chenon, A.; Godard, V.; Labia, R.; Nicolas, J.C. Antimicrob. Agents Chemother. 34, 1444-1446, 1990
A;Title: Nucleotide sequence of SHV-2 beta-lactamase gene.
A;Reference number: A60679; MUID:90351141; PMID:2201259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 beta-lactamase (EC 3.5.2.6) SHV-2 precursor - Salmonella typhimu
C;Species: Salmonella typhimurium
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change
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                            GQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGPK 121
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GDEQLERKIHYROODLVDYSPVSEKHLADGMTVGELCAAAITMSDNSAANLLLATVGGPA 142
                                                                                                             POPLEQIKQSESQLSGRVGMIEMDLASGRTLTAWRADERFPMMSTFKVVLCGAVLARVDA
                                                                                                                                       PETLVKVKDABDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRIDA
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                                                                                                                                                                                                                       71.7%; Score 552; DB 2; Length 286; 70.3%; Pred. No. 1.7e-45; tive 21; Mismatches 23; Indels
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Pred. No. 1.7e-45;
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C;Species: Escherrer
C;Date: 01-Dec-1989
C;Accession: S02434
RESULT 15
A60448
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A; Residues: 1-265 < BAR>
C; Superfamily: beta-lactamase I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Barthelemy, M.; Peduzzi, J.; Yaghlane, H.B.; Labia, R. FEBS Lett. 231, 217-220, 1988
A;Title: Single amino acid substitution between SHV-1 beta-lactamase and cefotaxime-hydx A;Reference number: S02434; MUID:88196385; PMID:3129309
A;Accession: S02434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Barthelemy, M.; Peduzzi, J.; Labia, R.
Blochem. J. 251, 73-79, 1988
A;Title: Complete amino acid sequence of p453-plasmid-mediated A;Reference number: S00464; MUID:88268817; PMID:3260490
A;Accession: S00464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       beta-lactamase (EC 3.5.2.6) SHV-2 - Escherichia coli
C;Species: Escherichia coli
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N;Alternate names: beta-lactamase PIT-2; beta-lactamase SHV-1
C;Species: Escherichia coli
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1993
C;Accession: S00464
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A; Residues: 1-265 <BAR>
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Best Local S
Matches 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Keywords: antibiotic resistance; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Genome: plasmid
;Superfamily: beta-lactamase I
;Keywords: antibiotic resistance; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                 Match 71.2%; Score 548; DB 2; Length 265 Local Similarity 70:3%; Pred. No. 3.8e-45; es 104; Conservative 21; Mismatches 23; Indels
                                                                                             122 ELTAFLHNMGDHVTRLDRWEPELNEAIP 149
||||| :||:|||||| ||||1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 GLTAFLRQIGDNVTRLDRWETELNEALP 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 ELTAFLHNMGDHVTRLDRWEPELNEAIP 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 GDEQLERKIHYRQQDLVDYSPVSEKHLADGMTVGELCAAAITMSDNSAANLLLITAVGGPA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 GQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGFK 121
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                                                                                                                                                                                                                                                                                                   POPLEOIKLSESOLSGRVGMIEMDLASGRTLTAWRADERFPMMSTFKVVLCGAVLARVDA
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                                                                                                                                                                                                GDEQLERKIHYRQQDLVDYSPVSEKHLADGMTVGELCAAAITMSDNSAANLLLTAVGGPA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 265;
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Search completed: June 10, Job time: 11.8657 secs

2005, 10:58:46

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A; Molecule type: protein
A; Residues: 1-265 < PBD>
A; Cross-references: UNIPROT: P37323
C; Superfamily: Beta-lactamase I
C; Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           beta-lactamase (EC 3.5.2.6) CAZ-5 - Klebsiella pneumoniae (strain 210-2) C;Species: Klebsiella pneumoniae C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 16-Aug-2004 C;Accession: A60448
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A;Accession: A60448
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Antimicrob. Agents Chemother. 33, 2160-2163, 1989
A;Title: Structural features related to hydrolytic activity against ceftazidime of plasmi
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                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                      Best Local Similarity
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  122
                                           122 ELTAFLHNMGDHVTRLDRWEPELNEAIP 149
                                                                                                                                                                                                                                                                                104; Conservative
                                                                                           62
                                                                                                                   62 GQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGFK 121
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                                                                                         GLTAFLRQIGDNVTRLDRWETELNEALP 149
                                                                                                                                                                                  71.2%; Score 548; DB 2; Length 265; 70.3%; Pred. No. 3.8e-45;
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Run on:
     2255432100654
2255432100654
2255432100654
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                                                                                                                                                                                                                                                                                                                                                                               Score
     Query
Match
    1000.00
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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               US-07-721-775A-2
US-08-339-658-2
US-09-263-933-7
US-09-263-933-14
US-09-263-933-21
US-09-263-933-21
US-09-919-901-7
US-09-919-901-21
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US-09-025-769B-390
US-09-490-070A-285
US-09-490-070A-390
US-09-490-070A-398
US-09-490-070A-398
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Sequence 2, Appli
Sequence 7, Appli
Sequence 14, Appli
Sequence 21, Appl
Sequence 25, App
Sequence 362, App
Sequence 14, Appl
Sequence 17, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 265, App
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Sequence 265, App
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Sequence 14, Appli
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Sequence 21, Appli
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Sequence 285, App
Sequence 362, App
Sequence 362, App
Sequence 363, App
Sequence 285, App
Sequence 285, App
Sequence 300, App
Sequence 300, App
Sequence 298, App
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1 HPETLYKYKDAEDQLGARVGYIELDLNSGKILE 	Query Match 100.0%; Score 885; DB 1; Length Best Local Similarity 100.0%; Pred. No. 3.7e-96; Matches 172; Conservative 0; Mismatches 0; Indels	о і	•	US-07-721-775A-2 ; Sequence 2, Application US/07721775A ; Patent No. 5180666 ; Patent INFORMATION: APPLICANT: States, J. Christopher APPLICANT: Hines, Ronald N. APPLICANT: No. 5180666ak, Raymond F. TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL NUMBER OF SEQUENCES: 2 CONDESSED NUMBERS.	RESULT 1	28 885 100.0 299 4 US-09-490-153-300 29 885 100.0 299 4 US-09-490-324-285 30 885 100.0 299 4 US-09-490-324-298 31 885 100.0 299 4 US-09-490-324-298 31 885 100.0 299 4 US-09-263-933-9 32 885 100.0 2307 3 US-09-263-933-9 34 885 100.0 2307 3 US-09-263-933-9 35 885 100.0 2307 4 US-09-919-901-2 36 885 100.0 2307 4 US-09-919-901-16 37 885 100.0 2307 4 US-09-919-901-16 38 815 100.0 2307 4 US-09-919-901-16 39 885 100.0 2307 4 US-09-19-966-2 39 885 100.0 2307 4 US-10-191-966-2 40 885 100.0 2307 4 US-10-191-966-16 41 884 99.9 286 4 US-10-231-013-9 42 884 99.9 1293 4 US-09-364-425B-57 48 884 99.9 1293 4 US-09-364-425B-57 48 884 99.9 1293 4 US-09-364-425B-57
SFRPEERFPMMSTFKVLLCGAVLSRID 60 	h 286; ls 0; Gaps 0		ton			Sequence 300, App Sequence 285, App Sequence 298, App Sequence 300, App Sequence 2, Appli Sequence 9, Appli Sequence 2, Appli Sequence 2, Appli Sequence 16, Appli Sequence 9, Appli Sequence 292, Appli Sequence 292, Appli Sequence 27, Appli

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84 61

AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120

AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP

143

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TELEFAX: (313) 689-4071
; INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
TYPE: amino acid
; TYPE: amino acid
; TYPE: TYPE: protein
US-08-339-658-2
RESULT 3
US-09-263-933-7
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,658
FILING DATE: 15-NOV-1994
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION OPERCHON
APPLICATION NUMBER: US 07/990,295
FILING DATE: 09-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-31WSU
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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APPLICANT: States,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reising, Ethington, Barnard, Perry & Milton
STREET: P.O. Box 4390
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TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL
                                                                                                                                                                                                                                                                                                                                                                                                / Match 100.0%; Score 885; DB 1; Length 286; Local Similarity 100.0%; Pred. No. 3.7e-96; nes 172; Conservative 0; Mismatches 0; Indels
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                                                                                                        KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGE 195
                                                                                                                                                      KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGE 172
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; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-263-933-7
                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0.125-0.005A CURRENT APPLICATION NUMBER: US/09/263,933 CURRENT FILING DATE: 1999-03-08 EARLIER APPLICATION NUMBER: 09/129,611 EARLIER APPLICATION NUMBER: 09/129,611 EARLIER FILING DATE: 1998-08-05 NUMBER: Patentin DATE: 1998-08-05 NUMBER: Patentin Ver. 2.0 SEQ ID NO 14 LENGTH: 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0.125-0.005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1999-08-05
NUMBER OF SEQ ID NOS: 33
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                Matches
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Patent No. 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Potts, Karen
                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                               Local
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                                                                                                                                                                                 Similarity
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AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 143
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                                                                                                                                                              Conservative
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                                                                                                                                                              100.0%; Score 885; DB 3;
100.0%; Pred. No. 3.7e-96;
tive 0; Mismatches 0;
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SEQ ID NO 21
LENGTH: 286
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Best Local Similarity
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CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: REPORTER GENE SYSTEM TITLE OF INVENTION: OF INHIBITORS OF THE FILE REFERENCE: 0125-0005A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
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APPLICANT:
APPLICANT:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION NUMBER: US/09/025,769B
APPLICATION NUMBER: US/09/025,769B
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                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Protein/(Poly)peptide libraries NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                      STREET: 1251 A
CITY: New York
STATE: New Yor
                                                                                                                                                                ZIP: 10021
                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                    USA
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Conservative 0
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Plueckthun, Andreas
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Pred. No. 3.7e-96;
); Mismatches 0;
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PRILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA;
APPLICATION NUMBER: EP 95 11 3021.0
PRILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                CITY: New York
STATE: New York
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                                                                                                                                                                                  APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                New York
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                                                                                                                                                                                                                                                                                                                                                                                   1251 Avenue
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US-09-025-769B-362

TOPOLOGY: linear MOLECULE TYPE: protein TYPE: amino acid

INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 286 amino acid

362:

286 amino acids

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US-09-919-901-14
; Sequence 14, Application US/09919901
; Patent No. 6599738
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COTHER INFORMATION:
US-09-919-901-7
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                                                                                                                                       RESULT 9
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Best Local Similarity
Matches 172; Conserv
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Patent No. 6599738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR PRIOR OF THE PRIO
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NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                              US-09-919-901-21
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APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Rober'
APPLICANT: Patick, Amy K.
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LENGTH: 286
TYPE: PRI
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                   SEQ ID NO 21
LENGTH: 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
  Matches 172;
                                          Query Match
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APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-005A
CURRENT APPLICATION: NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR FILING DATE: 1999-02-08
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APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR PILING DATE: 1999-08-05
NUMBER OF SEQ ID NOS: 33
NUMBER OF SEQ ID NOS: 35
NUMBER OF SEQ ID NOS: 35
NUMBER OF SEQ ID NOS: 3.
                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/129,611 PRIOR FILING DATE: 1998-08-05
                                                                                                                    OTHER INFORMATION:
                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
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nes 172; Conserv
                      Local Similarity
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    Application US/09919901
6599738

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100.0%; Score 885; DB 4; llarity 100.0%; Pred. No. 3.7e-96; Conservative 0; Mismatches 0;
                                          Length 286;
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  Indels 0;
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Gaps
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1 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID

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144

KELTAFLHNMGDHVTRLDRWEPELNEAI PNDERDTTMPVAMATTLRKLLTGE

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; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-490-070A-265
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US-09-490-070A-265
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202) 912-20 INFORMATION FOR SEQ ID NO: 265: SEQUENCE CHARACTERISTICS:
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Moroney, Simon
Pluecktum, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTED. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 37629-0005 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20006
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                172;
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KELTAFLHNMGDHYTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGE 172
                                                                                          AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                                                                                          HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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                                                                AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acids
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                                                                                                                                                                                                                             100.0%; Score 885; DB 4; ilarity 100.0%; Pred. No. 3.7e-96; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                    Length 286;
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US-09-490-070A-362
                                                                                                                                                                                                                                       Matches 172;
                                                                                                                                                                                                                                                                            Query Match
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 362,
                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (202) 912-2
TELEPAX: (202) 912-20;
INFORMATION FOR SEQ ID NO: 362:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Versi
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 362:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Protein/(Poly)peptide libraries NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
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144
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                                                                                                                  61 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                                                                                                 1 HPETLYKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60
                             KELTAFLHIMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLIGE 172
                                                                             AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                                                          HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
KELTAFLHNMGDHVTRLDRWEPELNEAI PNDERDTTMPVAMATTLRKLLTGE
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 286 amino acids
                                                                                                                                                                                                                                     100.0%; ilarity 100.0%; Conservative 0
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Plueckthun, Andreas
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Ilag, Vic
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Pred. No. 3.7e-96;
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195
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US-09-490-153-265
; Sequence 265, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:

RESULT 13

APPLICANT: Knappik, Achim

Moroney, Simon
Plueckthun, Andreas Ge, Liming Moroney, Simon Pack, Peter Ilag, Vic

NUMBER OF SEQUENCES:

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RESULT 14
US-09-490-153-362
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                                                                                                                                                   Sequence 362, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
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Best Local Similarity
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TELEPAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION NUMBER: US/09/490,153
PALICATION NUMBER: US/09/490,153
PILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-AUG-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
APTORNEY/ACENT INFORMATION:
NAME: JEGGE P 43107.17 FGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
TITLE OF
                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Protein/(Poly)peptide libraries NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                                                                                                                                                                      121 KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
INVENTION: Protein/(Poly)peptide libraries
                                                                                                                                Knappik, Achim
                    Plueckthun, Andreas
                                                                                  Pack, Peter
Ilag, Vic
                                                                Ge, Liming
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                                           Simon
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Pred. No. 3.7e-96;
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; TOPOLOGY: Innear;
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 362:
US-09-490-153-362
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US-10-191-966-7
                  GENERAL INFORMATION:

APPLICANT: Potts, Karen E.

APPLICANT: Jockson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/99/263,933
PRIOR APPLICATION NUMBER: US/99/263,933
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
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Matches
                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/490,153
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGE 172
                                                                                                                                                                                                                                                                                                                                                                                7, Application US/10191966
5. 6790612
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PatentIn Ver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 286 amino acids
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100.0%; Pred. No. 3.7e-96;
tive 0; Mismatches 0;
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; SEQ ID NO 7
; LENGTH; 286
; TYPE; PRT
; ORGANISM: Artificial Sequence
; PEATURE:
; ORGANISM: Artificial Sequence
; PEATURE I PAGE
; ORGANISM: Artificial Sequence
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Result
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Perfect score:
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         B B
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573
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    No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.

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Copyright (c) 1993 - 2005 Compugen Ltd.
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Bla protein - Salm
beta-lactamase (EC
probable Beta lact beta-lactamase (EC beta-lactamas
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C;Superfamily: beta-l;
C;Keywords: hydrolase
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A; Residues: 1-286 <WAC>
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41.4 306 2 G69674 41.4 311 2 JN0520 40.7 305 2 A57002 40.7 305 2 A57002 40.7 305 2 A57030 40.4 306 2 S47330 39.6 288 2 JQ1136 39.6 291 2 JP0074 39.5 305 1 C45822 39.4 294 2 S44080 39.3 263 2 S23929 39.2 304 2 A49789 39.2 304 2 A49789 39.0 311 1 S03701 39.0 314 1 PNSMIU	41.4 311 2 JN0520 41.4 311 2 JN0520 40.7 305 2 A511.56 40.7 305 2 A60.680 40.7 305 2 A60.680 40.4 306 2 S47330 39.6 28 1 JQ1136 39.6 291 2 JQ1136 39.6 291 2 JP0074 39.5 305 1 C45822 39.4 294 2844880 39.3 263 2 S23929 39.3 263 2 S23929 39.2 304 2 A49789 39.3 304 2 A49789 39.0 311 1 S02714 39.0 314 1 PNSMIU	45	44	3	42	41	40	39	38	37	36	35	34	ω ω	32	31	٥
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2 G69674 2 JN0520 2 A61156 2 A57002 2 A57002 2 A60680 2 JQ1136 2 JQ1136 2 JF0074 1 C45822 2 S23929 2 S23929 2 A49789 2 S23929 2 A49789 1 S02714 1 S02714	2 G69674 beta-lactamase 2 JN0520 beta-lactamase 2 A61156 beta-lactamase 2 A57002 beta-lactamase 2 A60680 beta-lactamase 2 S47730 beta-lactamase 2 UP0074 beta-lactamase 2 UP0074 beta-lactamase 2 UP0074 beta-lactamase 2 S44080 beta-lactamase 2 S23929 beta-lactamase 2 S23929 beta-lactamase 3 S2301 beta-lactamase 3 S02714 beta-lactamase 1 S02714 beta-lactamase 1 S02714 beta-lactamase	39.0	39.0	39.2	39.2	39.3	39.4	39.5	39.6	39.6	40.4	40.7	40.7	40.7	41.4	41.4	41.9
949942 G69674 JN0520 A61156 A51002 A60680 947330 JQ1136 JP0074 C45822 S44080 S23929 A49789 A49789 A35001 S02714	## 1972	314	311	304	304	263	294	305	291	288	306	305	305	305	311	306	500
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		ק	. 6.														

ALIGNMENTS

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RESULT 2
$47061
$47061
beta-lactamase (BC 3.5.2.6) - phage phi-X174
C;Species: phage phi-X174
C;Date: 13-Jan-1995 #sequence_revision 13-Jan
C;Accession: $47061
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-286 <HEN>
A;Cross-references: UNIPROT:Q38058; EMBL:Z35638; NID:g520996; PIDN:CAA84692.1; PID:g52099
                                                                                                          R;Henrich, B.; Schmidtberger, B. submitted to the EMBL Data Library, A;Description: A variant of phiX174 A;Reference number: S47060 A;Accession: S47061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;WACH, A.; BRACHAT, A.; ALBERTISEGUI, Yeast 13, 1065-1075, 1997
R;Title: Heterologous HIS3 marker and CA;Reference number: Z09587
A;Accession: T51301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            beta-lactamase (EC 3.5.2.6) - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C;Accession: T51301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated
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Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                             KELTAFLHNMGDHVTRLDRWEPELNEA I PNDERDTTMPVAMATTLRKLLTGE
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Pred. No. 4.1e-74;
                                                                                                                                                              July 1994
gene B-based
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                                                                                                                                                                                                                                                                      13-Jan-1995 #text_change 09-Jul-2004
                                                                                                                                                                    positive selection vectors with enhanced
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RESULT 3
S41975
                                                                                                                                                                                                                                   beta-lactamase (EC 3.5.2.6) precursor - Escherichia coli plasmids N;Alternate names: beta-lactamase TEM-6 (for blaT-6 DNA); penicillinase C;Species: Escherichia coli C;Date: 30-Nov-1980 #sequence revision 01-Sep-1981 #text_change 16-Aug-2004 C;Accession: A93821; A93820; A35387; S24415; A01005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Title: Universal beta-galactosidase cloning vectors for A;Reference number: A57991; MUID:95011660; PMID:7926839 A;Accession: S41975
A;Cross-references: UNIPROT:P00810; GB:V00613; GB:J01832; A;Experimental source: plasmid pBR322 R;Ambler, R.P.; Scott, G.K.
proc. Natl. Acad. Sci. U.S.A. 75, 3732-3736, 1978
                                                                                                                                                                                           R;Sutcliffe, J.G. Proc. Natl. Acad. Sci. U.S.A. 75,
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A;Residues: 1-286 <KAE>
A;Cross-references: EMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Kaestner, K.H.; Montoliu, L.; Kern, H.; Thulke, M.; Schutz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               beta-lactamase (EC 3.5.2.6) precursor - C;Species: synthetic
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                                                                                    A; Molecule type: DNA
A; Residues: 1-286 <SUT>
                                                                                                                                                 A; Title: Nucleotide sequence A; Reference number: A93821; N
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                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Date: 25-Dec-1994 #sequence_revision;Accession: S41975
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                                                                                                                                 Accession: A93821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Keywords: hydrolase
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MUID:79012484; PMID:358200
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Pred. No. 4.1e-74;
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Pred. No. 4.1e-74;
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                      A; Molecule type: DNA
A; Residues: 1-286 < R
                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
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R;Sutcliffe, J.G.
Cold Spring Harb. Symp. Quant. Biol. 43, 77-90, 1979
A;Title: Complete nucleotide sequence of the Escherichia
A;Reference number: A90923; MUID:80002802; PMID:383387
A;Contents: annotation
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R;Kornacki, J.A.; Burlage, R.S.; Figurski, D.H.
J. Bacteriol. 172, 3040-3050, 1990
A;Title: The kil-kor regulon of broad-host-range plasmid RK2: nucleotide sequence,
A;Reference number: A35387; MUID:90264294; PMID:2160936
A;Accession: A35387
                       R:Taylor, J.; Stearman, R.S.; Uratani, B.B.
Plasmid 29, 241-244, 1993
A;Tille: Development of a native plasmid as
A;Reference number: I40904; MUID:93361581; I
                                                                                                                          A;Note: cloning vector pCG1408 engineered and expressed in Clavibacter xyli subsp. cynodc C;Date: 15-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Oct-2000 C;Accession: 140905
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F;75-121/Disulfide bonds: #status predicted
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A;Cross-references: EMBL:X57972; NID:g41816; PIDN:CAA41038.1;
A;Experimental source: ISI-like blaf-6 DNA
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A;Residues: 182-286 <KOR>
A;Cross-references: GB:M32794; NID:g152521; PIDN:AAA26408.1;
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A;Reference number: A93820; MUID:79012483; PMID:358199
A;Accession: A93820
A;Molecule type: protein
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A;Title: An IS1-like element is responsible for high-level synthesis of extended-spectrum
A;Reference number: S24415; MUID:92166702; PMID:1665171
A;Accession: I40905
                                                                                                                                                                                                         C; Species: synthetic
                                                                                                                                                                                                                                beta-lactamase
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R;Goussard, S.; Sougakoff, W.; Mabilat, C.; Bauernfeind, A.;
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                                                                                                                                                                                                                                (EC 3.5.2.6) -
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Pred. No. 1.2e-73
                            pMID:7689234
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-286 <RES>

EMBL:U21228; NID:g885956; PIDN:AAA70411.1; PID:g885958

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RESULT 7
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C;Superfamily: beta-lactamase I
C;Keywords: antibiotic resistance; hydrolase
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A;Molecule type: DNA
A;Residues: 1-286 <MAB>
A;Cross-references: UNIPROT:P00810;
C;Genetics:
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A;Title: A new example of physical linkage between Tn1 and A;Reference number: S30112; MUID:93062798; PMID:1331747
A;Accession: S30113
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Pred. No. 6.6e-73;
3; Mismatches 1
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beta-lactamase (EC 3.5.2.6) TEM-1 - Klebsiella pneumoniae transposon Tn1331 (;Species: Klebsiella pneumoniae (;Species: Klebsiella pneumoniae (;Species: Klebsiella pneumoniae (;Species: Labr-1996 #sequence revision 19-Apr-1996 #text_change 09-Jul-2004 (;Accession: S60311; B37392; P00498 R;Chanal, C.; Poupart, M.C.; Sirot, D.; Labia, R.; Sirot, J.; Cluzel, R. Antimicrob. Agents Chemother. 36, 1817-1820, 1992 A;Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase gene A;Reference number: S60310; MUID:93037315; PMID:1416873 A;Accession: S60311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
S60311
A;Title: Sequencing and expression of aadA, bla, and tnpR A;Reference number: A37392; MUID:91172904; PMID:1963948 A;Accession: F37392
                                                                          A;Cross-references: UNIPROT:Q99224; EMBL:X65253; NID:g296953; R;Tolmasky, M.E. Plasmid 24, 218-226, 1990
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A;Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes. A;Reference number: S60310; MUID:93037315; PMID:1416873
A;Accession: S60310
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S60310
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                                                                                                                                                         A;Residues: 1-286 <CHA>
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Pred. No. 2.3e-72;
3; Mismatches 2
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A; Gene:
C; Superf
C; Keywor
C;Species: Klabsiella pneumoniae
C;Date: 21-Nov-1993 #sequence revision 10-Nov-1995 #text_change 15-Oct-1999
C;Accession: S16146; A35395; S18767
C;Podbielski, A.; Schoenling, J.; Melzer, B.; Warnatz, K.; Leusch, H.G.
J. Gen. Microbiol. 137, 569-578, 1991
A;Ritle: Molecular characterization of a new plasmid-encoded SHV-type beta-lactamase
A;Reference number: S16146; MUID:91237320; PMID:2033379
A;Accession: S16146
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A;Cross-references: GB:M55547; NID:g155010; PIDN:AAA98408.1; PID:g155016
C;Genetics:
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Plasmid 27, 220-230, 1992
A;Title: Complete nucleotide sequence and gene organization A;Reference number: JQ1538; MUID:92383313; PMID:1325061
A;Accession: JQ1546
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JQ1546
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A;Cross-references: UNIPROT:Q8L2F9
C;Genetics:
A;Genome: plasmid
C;Superfamily: beta-lactamase I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             la protein - Salmonella typhimurium plasmid NTP16;Alternate names: beta lactamase homolog;Species: Salmonella typhimurium
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Pred. No. 2.3e-72;
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C;Keywords: antibiotic resistand
F;1-21/Domain: signal sequence:
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C;Superfamily: beta-lactamase
C;Keywords: antibiotic resista
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A; Residues: 1-286 < GAR>
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69.6%;
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R;Lee, K.Y.; Hopkins, J.D.; Syvanen, M.
J. Bacteriol. 172, 3229-3236, 1990
A;Title: Direct involvement of IS26 in an antibiotic resistance
A;Reference number: A35395, MUID:90264317, PMID:2160941
A;Accession: A35395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Garbarg-Chenon, A.; Godard, V.; Labia, R.; Nicolas, J.C. Antimicrob. Agents Chemother. 34, 1444-1446, 1990
A;Title: Nucleotide sequence of SHV-2 beta-lactamase gene. A;Reference number: A60879; MUID:90351141; PMID:2201259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           beta-lactamase (EC 3.5.2.6) SHV-2 precursor - Salmonella typhimurium plasmid C;Species: Salmonella typhimurium C;Species: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Aug-2004 C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Aug-2004
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A;Residues: 1-30,'L',32-286 <LEE>
A;Cross-references: GB:X62115; NID:g48988; PIDN:CAA44025.1;
A;Experimental source: plasmid BWH77
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A;Experimental source: plasmid pZMP1
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                                  GQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGFK 121
                                                                                                             POPLEQIKQSESQLSGRVGMIEMDLASGRTLTAWRADERFPMMSTFKVVLCGAVLARVDA
                                                                                                                                                  PETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRIDA 61
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Pred. No. 2.1e-50;
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Pred. No. 2.1e-50;
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RESULT 15
A60448
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C;Accession: S02434
R;Barthelemy, M.; P
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Biochem. J. 251, 73-79, 1988
A;Title: Complete amino acid sequence of p453-plasmid-mediated
A;Reference number: S00464; MUID:88268817; PMID:3260490
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A;Title: Single amino acid substitution between SHV-1 beta-lactamase and cefotaxime-hydr
A;Reference number: S02434; MUID:88196385; PMID:3129309
A;Accession: S02434
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C;Species: Escherichia coli
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C;Superfamily: beta-lactamase I
C;Keywords: antibiotic resistance; hydrolase
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A;Molecule type: protein
A;Residues: 1-265 <BAR>
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C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1993
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: beta-lactamase I
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beta-lactamase (EC 3.5.2.6) CAZ-5 - Klebsiella pneumoniae (strain 210-2) C;Species: Klabsiella pneumoniae. (c;Species: Klabsiella pneumoniae. (c;Date: 03-Max-1993 #sequence_revision 03-Max-1993 #text_change 16-Aug-2004 C;Accession: A60448 R;Peduzzi, J.; Barthelemy, M.; Tiwari, K.; Mattioni, D.; Labia, R. Antimicrob. Agents Chemother. 33, 2160-2163, 1989 A;Structural features related to hydrolytic activity against ceftazidime of plasmi A;Accession: A60448; MUID:90146269; PMID:2694955 A;Accession: A60448 MUID:90146269; PMID:2694955 A;Status: preliminary
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C;Superfamily: Beta-lactamase I
C;Keywords: hydrolase
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                                                                                           122 BLTAFLHNMGDHVTRLDRWEPELNBAIPNDBRDTTMPVAMATTLRKLLTGE 172
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69.6%; Pred. No. 4.6e-50;
ative 23; Mismatches 29
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Maximum DB
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SSECTION

Q6WWY4
Q6WWY4;
Q6WWY4;
Q6WWY4;
Q5-WUL-2004 (TERMBLrel. 27, Created)
Q5-UUL-2004 (TERMBLrel. 27, Last sequence update)
Q5-UUL-2004 (TERMBLrel. 27, Last annotation update)
Beta-lactamase (Fragment).
Name=blaTEM;
Hafnia alvei.

update)

RESULT Q6WWY4	문 &	A 4	B 8	Ma B Q	SOT	R R R	75 K	B R R	2×000		RESULT Q6WWY5								
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05-JUL-2004 (TrEMBLrel.
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Submitted (APR-2004) to the
EMBL; AY265886; AAP93844.1;
                                                                                                                                                                                                                                                                                                                               InterPro; IPR001466; Beta lactamase.
InterPro; IPR000871; Beta lactamase A.
Pfam; PF00144; Beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Klebsiella.
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Enterobacteriaceae; Hafnia
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241 AA;
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232 AA;
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InterPro; IPR000871; Beta_lactamase_A.
Pfam; PF00144; Beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE_A; 1.
NON_TER 1 1
NON_TER 242 242
TISSUE-First leaf;
Jansen C., Korell M., Eckey C., Biedenkopf D.,
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ (
EMBL; AJ717739; CAG30723.1; -.
HSSP; P00807; 1ALQ.
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Submitted (APR-2004) to the
EMBL; AY265887; AAP93845.1;
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Q38058;
01-NOV-1996
                                                                                                                                                                                                                                                   Henrich B., Schmidtberger B.;

"A variant of phiXI74 gene E-based positive selection vectors with enhanced lytic potential.";

Gene 154:51-54(1995).

EMBL; Z35638; CAA84692.1; -.

EMBL; Z35638; CAA84692.1; -.

BIR; S47061; S47061.

HSSP; Q9R435; 1HTZ.

InterPro; IPR001466; Beta lactamase.

InterPro; IPR000871; Beta lactamase.

InterPro; IPR000871; Beta lactamase; 1.
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01-NOV-1996 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
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PRINTS; PR00118; BLACTAMASEA.
PROSITS; PS00146; BETA_LACTAMASE_A;
                                                                                                                                                                                                                PRINTS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA LACTAMASE A; 1.
SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beta lactamase.
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MEDLINE=95172401; PubMed=7867948;
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InterPro; IPR000871; Beta_lactamase_A.
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                 KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLIGE 172
                                                                  AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 885; DB 2;
larity 100.0%; Pred. No. 4.7e-69;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31371 MW;
                                                                                                                                                                       100.0%; Score 885; DB 2; 100.0%; Pred. No. 4.7e-69;
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24,
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                                                                                                                                                           Mismatches
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annotation update)
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Matches 172
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SEQUENCE FROM N.A.

PLASMID=J3356/pOX7/3, and J3356/POX7/1;

MEDLINE=96422755; PubMed=8825372; DOI=10.1006/plas.1995.0005;

Meddham C., Noble W.C., Dyke K.G.;

"The staphylococcal insertion sequence IS257 is active.";

Plasmid 34:198-205(1995).

EMBL; U36912; AAB39957.1; --

EMBL; U36911; AAB39957.1; --

InterPro; IPR001466; Beta_lactamase.

InterPro; IPR000871; Beta_lactamase_A.
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                                                                                                                                                                                             MEDLINE=97074643; PubMed=8917070; DOI=10.1016/0378-1119(96)00114-X; MEDLINE=97074643; PubMed=8917070; DOI=10.1016/0378-1119(96)00114-X; Serebrijski I.G., Vassin V.M., Tsygankov Y.D.; "Two new members of the BioB superfamily: cloning, sequencing and expression of bioB genes of Methylobacillus flagellatum and Corynebacterium gultamicum."; Gene 175:15-22(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methylobacillus flagellatum.
Bacteria; Proteobacteria; Betaproteobacteria; Methylophilales;
Methylophilaceae; Methylobacillus.
NCBI_TaxID=405;
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
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Plasmid J3356/pOX7/3,
Bacteria; Firmicutes;
                                 SEQUENCE FROM N.A.
Serebrijski I., Vassin V
Submitted (JUL-1995) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beta-lactamase.
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e EMBL/GenBank/DDBJ
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InterPro; IPR001466; Beta_lactamase.
InterPro; IPR000871; Beta_lactamase.
Pfam; PP001144; Beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE A; 1.
SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9
       "Molecular Characterization of Extended-Spectrum Produced by Clinical Isolates of Klebbiella pneum coli from a Korean Nationwide Survey."; J. Clin. Microbiol. 42:2902-2906(2004). EMBL; M74750; AAA24057.1; -- EMBL; Y12694; CAA73226.1; -- EMBL; AJ001614; CAA04868.1; -- EMBL; AV425988; AAQ95605.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid pRP4, and Plasmid pCAPs.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                        STRAIN=K12; PLASMID=pRP4;
Rondot S., Anthony K., Dubel
Little M., Breitling F.;
Submitted (APR-1997) to the
                                                                                                                                                                                                                   Schlieper D., \
Mueller-Hill B
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Submitted (AUG-1991) to the EMBL/GenBank/DDBJ databases
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STRAIN=K-12;
                                                                                                        Jeong S.H., Bae I.K.,
Kim Y.H., Jeong B.C.,
                                                                                                                                PubMed=15243036;
                                                                                                                                              SEQUENCE
                                                                                                                                                                                Escherichia
                                                                                                                                                                                          "A positive selection vector for cloning reaction fragments based on a lethal muta
                                                                                                                                                                                                                                      MEDLINE=98189310;
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                                                                                                                                                                    257:203-209(1998).
                                                                                                                                                                                                                             PubMed=9514792; DOI=10.1006/abio.1997.2558; Wilcken-Bergmann B., Schmidt M., Sobek H.,
                                                                                                        Lee J.H.,
Lee S.H.;
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                                                                                             Beta-Lactamases
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Q38212;
01-NOV-1996
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MEDLINE=86278026; PubMed=3525535;

Topal M.D., Badie J.S., Conrad M.;

"O-6-methylguanine mutation and repair is nonuniform:

"O-6-methylguanine with O-6-methylguanine.";

DNA most interactive with O-6-methylguanine.";

J. Biol. Chem. 261:9879-9885(1986).

EMBL; M14017; AAA32208.1; -.

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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Bacteriophage f1-R208 ampicillinase gene mutation.
Bacteriophage f1.
Viruses; ssDNA viruses; Inoviridae; Inovirus.
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GO; GO:0008800; F:beta-lactamase activity; GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR001466; Beta-lactamase.
InterPro; IPR000871; Beta-lactamase_A.
Pfam; PF00114; Beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
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PROSITE; PS00146; BETA LACTAMASE_A; 1.

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Pred. No. 9.6e-69;
1; Mismatches 1
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Pred. No. 4.7e-69;
Mismatches 0;
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Best Local Similarity
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Q6PRU7;
05-JUL-2004 (TrEMBLrel. 2;
05-JUL-2004 (TrEMBLrel. 2;
05-JUL-2004 (TrEMBLrel. 2;
Inhibitor-resistant TEM b
NON_TER
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SEQUENCE
                                                                               PRINTS; F
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q84H50 PRELIMINARY; PRT; 255 AA. Q84H50; 01-JUN-2003 (TrEMBLrel. 24, Created) 01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) TEM-117 beta-lactamase (Fragment).
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Submitted (WAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY583761; AA586427.1; -.
HSSP; P00807; 1ALQ.
InterPro; IPR001466; Beta_lactamase.
InterPro; IPR00147; Beta_lactamase_A.
Pfam; PF00114; Beta_lactamase_I.
PRINTS; PR00118; BLACTAMASEA.
                                                                                                                          InterPro; IPR001466; Beta lactamase. InterPro; IPR000871; Beta lactamase A. Pfam; PF00144; Beta-lactamase; 1.
                                                                                                                                                                                                            Box A.T.A., Paauw A., Leverstein-vanHall M.A.; Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AY130282; AAN05026.1; -. HSSP; Q9R435; 1HTZ.
                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
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                                                                         PR00118; BLACTAMASEA.; PS00146; BETA_LACTAMASE_A;
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232 AA;
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27, Last sequence update)
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beta-lactamase (Fragment).
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Pred. No. le-68;
l; Mismatches
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     DCBB28B65978C3A6 CRC64;
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RESULT

Q84H49

ID 4H49

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AC AC Q8

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RESULT 14
Q6FRU6
ID Q6FRU
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Best Local Simi
Matches 170;
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Best Local Sim
Matches 170;
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InterPro; IPRO0147; Beta_lactamase_A.
Pfam; PF00144; Beta_lactamase; 1.
PRINTS; PRO0118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE_A; 1.
NON_TER 1 1
NON_TER 261 261
SEQUENCE 261 AA; 28738 MW; 4F748F773
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Q84H49;
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05-JUL-2004 (TrEMBLrel. 27, I
05-JUL-2004 (TrEMBLrel. 27, I
TEM beta-lactamase (Fragment)
Acinetobacter sp. Ull.
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01-JUN-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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                                    Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Acinetobacter.
                                                                                                                                                                                                                                                                                 Q6PRU6;
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Enterobacteriaceae; Klebsiella.
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28738 MW; 4F748F7733A08CBB CRC64;
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98.8%;
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24, Last sequence update)
25, Last annotation updat
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Pred. No. 1.1e-68;
1; Mismatches 1
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Pred. No. 1.1e-68;
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databaвев.
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SEQUENCE FROM N.A.

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RESULT 15
QGQIVO
DGQIV
AC QGQIV
DT 05-JU
DT 05-J
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Matches 170; Conserva
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Best Local Similarity
Matches 170; Conservat
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PROSITE; PS00146; BETA_LACTAMASE_A; 1.
                                                                                                                                                                                                                                                                                                                               NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-ES-42, ES-46, ES-71, and ES-11;
STRAIN-ES-42, ES-46, ES-71, and ES-11;
Yatsuyanagi J., Saito S., Harata S., Suzuki N., Amano K.-I.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY538700; AAS46846.1; -.
EMBL; AY538701; AAS46847.1; -.
EMBL; AY538702; AAS46848.1; -.
EMBL; AY538698; AAS46844.1; -.
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001466; Beta_lactamase.
InterPro; IPR000871; Beta_lactamase_A.
Pfam; PF00144; Beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE_A; 1.
NON TER
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Serratia marcescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterobacteriaceae; Serratia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TEM-1 beta-lactamase (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGE 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRVD 71
                                                                                                                                            μ
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                                                                                                                   HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60
                                                                               HPETLVKVKDAEDQLGARVGYIELDLNSGKILESPRPEERPPMMSTFKVLLCGAVLSRVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 131
                      AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KELTAFLHINGGHVTRLDRWEPELNEAI PNDERDTTMPAAMATTLRKLLTGE
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264 AA;
                                                                                                                                                                                                                                                                                                                               281 281
281 AA; 30837 MW; C8934B9C696057BF CRC64;
                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hosseini-Mazinani S.M.;
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; 28986 MW; A4F071CF7489352C CRC64;
                                                                                                                                                                                                      99.4%; Score 880; DB 2; Length 281; 98.8%; Pred. No. 1.3e-68; tive 1; Mismatches 1; Indels
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144
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              KELTAFIHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGE 172
                                        KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPAAMATTLRKLLTGE 195
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Search completed: June 10, 2005, 10:57:02 Job time: 58.6231 secs

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Minimum DB
Maximum DB
                                                                                                                                                              Database
                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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A Geneseq_16Dec04:*
1: geneseqp1980s:*
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Gapop 10.0 ,
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925
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	ų	80	7	σ	σ	4	ω	N		Result No.
925	925	925	925	925	925	925	925	925	925	925	925	925	925	925	925	925	925	925	925	925	925	925	925	925	Score
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0		•	100.0	100.0	100.0	Query Match I
290	286	286	286	286	286	286	286	286	286	286	286	286	286	286	286	286	286	286	286	264	264	263	263	263	Length
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AAU23219	ADR70428	ADR70416	ADR70404	ADR70410	ADR70422	ABR43622	ABP55474	AAU75551	AAB31173	AAB50898	AAB10440	AAB10438	AAB10442	AAY08529	AAW18679	AAW16635	AAR96423 .	AAR97619	AAR31575	AAW18680	AAW16634	ADJ67709	AAB36692	AAB05544	ID
Aau23219 Novel hum	Adr70428 Vector pA	Adr70416 Vector pA	Adr70404 Vector pA		Adr70422 Vector pA	Cloni		Aau75551 celZ inte	Aab31173 Amino aci	Aab50898 Protein e	Aab10440 Expressio	Aab10438 Expressio	Aab10442 Expressio	Aay08529 Vector pA	Aaw18679 Secretory	Aaw16635 Beta-lact	Aar96423 Cytochrom	Aar97619 Secretory	Aar31575 Ampicilli	Aaw18680 Intracell	Aaw16634 Beta-lact	_	Aab36692 Escherich	Aae05544 E. coli m	Description

13-JAN-2000; 15-MAR-2000;

2000US-0175968P. 2000US-00526106.

16-JAN-2001; 2001WO-US001651

WO200151629-A2

45	44	43	42	41	40	39	38	37	36	35	34	S S	32	31	30	29	28	27	26
920	920	920	924	924	924	924	924	925	925	925	925	925	925	925	925	925	925	925	925
99.5		99.5			99.9	99.9	99.9			100.0		100.0				100.0			100.0
265	265	265	1967	1293	1293	872	286	2761	2307	2307	2307	1277	1088	1031	585	408	327	327	290
N	N	N	0	7	7	7	N	N	w	w	w	N	N	ហ	σ	σ	N	N	4
AAW48613	AAY08232	AAY08234	ABB82793	ADH14284	ADC22811	ADK65686	AAY06551	ADH11249	AAY70066	AAY70065	AAY70064	AAR52701	AAR88636	ADI46109	ADA67747	ABR55981	AAW18681	AAW16636	AAM84362
Aaw48613	Aay08232	Aay08234	Abb82793	Adh14284	Adc22811	Adk65686	Aay06551	Adh11249	Aay70066	Aay70065	Aay70064	Aar52701	Aar88636	Adi46109	Ada67747	Abr55981	Aaw18681	Aaw16636	Aam84362
Escherich	E. coli R	E. coli R	Amino aci	Vector pc	Human G p	E coli cl	Escherich	Vertebrat	Recombina	Recombina	Recombina	Plasmid p	Plasmid p	Single st	Beta-lact	hCG beta-	Membrane-	Beta-lact	Human 1mm

ALIGNMENTS

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RESULT 1
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XX AAEO
XX AAEO
XX Inte
XW Circ
XW C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interaction-dependent enzyme association; IdEA system; biosensor; circularly permutated interaction-activated protein; marker protein; type A beta-lactamase; TEM-1 beta-lactamase; protein-protein interaction; therapeutic; drug screening; thioredoxin; ampicillin resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B. coli mature TEM-1 beta-lactamase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cleavage-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149. .150
                                                                                                                                                                                                                                                                                                                                                                                                                               189. .204
/note= "Inter-sub-domain loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172. .173
                                                                                                                                                                                                                                                                                           /note= "Break-point between alpha and 228. .229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "Break-point between alpha"
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38. .39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "Break-point between alpha and omega fragments"
                                                                                                                                                                                                                                                                note=
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                                                                                                                                                                                                                                                                                                                                        Matches 181;
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 38; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interaction-dependent enzyme association systems for detecting interactions between two or three polypeptides, especially in human therapeutics, diagnostics or prognostics, comprise circularly permutated
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-451857/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PANO-) PANORAMA RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to new interaction-dependent enzyme association
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                                                                                                                                                                                                                                                                                                                                                                Similarity
Q 181
                                                                                                                                                                                                                                                                                HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                                     0 181
                                                                               KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ
                                                                                                          KELTAFIHNMGDHVTRLDRWEFELNEAIPNDERDTTMFVAMATTLRKLLTGELLTLASRQ
                                                                                                                                                                    AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                                                                                                              AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                                                                                                                                                                        HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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                                                                                                                                                                                                                                                                                                                                        Score 925; DB 4;
Pred. No. 2.9e-94;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                Length 263;
                                                                                                                                                                                                                                                                                                                                          Indels
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RESULT 2
AAB36692
ID AAB36932
XX AAB3
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R 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a fragment complementation system (I) CC which comprises a first oligopeptide (OP1) containing an N-terminal CC fragment with a C-terminal break point and a second oligopeptide (OP2) CC comprising a C-terminal with a N-terminal breakpoint, in which the C and CC reassemble to form a functionally reconstituted MP. Methods from the CC protein interactions in a sample, identifying oligopeptide interactions for memoraphous that brind to an extracellular domain of a transmembrane protein and a polypeptide, for complicated signal transducers, forming a protein and a polypeptide, for complated signal transducers, forming a enzyme complementation system for selecting simultaneous incorporation of multiple genetic elements into a flost the lost cell and for activating a beta-lactam derivative of an antitumour CC compound in a host who is in need of it. The present sequence represents CC exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                     Matches 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel fragment complementation system to identify interactions between polypeptides comprises fragment pairs having first and second members that reassemble into a marker protein which has a directly detectable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB36692;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 2; 94pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Balint RF, Her J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAY-1999; 99US-0135926P.
13-JAN-2000; 2000US-0175968P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-MAR-2000; 2000WO-US007108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200071702-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interaction-activated protein; beta-lactamase; protein interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli mature TEM-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PANO-) PANORAMA RES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-032034/04.
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                                                     KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 180
                                                                                                                 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                                                       AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLITTIGGP 120
                                                                                                                                                                                                                                          HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPWMSTFKVLLCGAVLSRID
                                                                                                                                                                                                                                                                             HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                               Score 925; DB 4;
Pred. No. 2.9e-94;
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TTMPVAMATTLRKLLTGELLTLASRQ
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 263;
                                                                                                                                                                                                                                                                                                                                                                        Indels
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RESULT 3
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CC terminal fragment each are derived from a marker protein and reassemble Ct to form a functionally reconstituted marker protein and reassemble Ct to form a functionally reconstituted marker protein. (I) is useful for CC selecting simultaneous incorporation of multiple genetic elements into a CC to host cell, and activating a beta-lactam derivative of an anti-tumour CC compound in a host. The method described is useful for identifying a CC second oligopeptide to which a first oligopeptide binds, involving co-CC expressing the first and second oligopeptides. Binding of the first CC oligopeptide to the second oligopeptide results in the functional CC reassembly of the marker protein. The method is also useful for CC dentifying oligopeptide interactions between two different proteemes; CC and identifying epitopes that bind to an immunoglobulin variable region. CC (I) or an expression casette (II), encoding a selectable N or C-terminal peptide, is useful for identifying interactions between an extra cellular CC domain of a transmembrane protein and a polypeptide, where the CC (II) is useful for high-throughput identification of compound that CC inhibit phosphorylation-regulated cell signal transducers. (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention describes a fragment complementation system (I) comprising a first oligopeptide having an N-cerminal fragment with a C-terminal break-point, and a second oligopeptide having a C-terminal fragment with a N-terminal break-point, where the N-terminal fragment and the C-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fragment complementation system for detecting immunoglobulin epitope, has first oligopeptide containing N-terminal fragment with C-terminal break-point, second oligopeptide containing C-terminal fragment with N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 2; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-203222/19.
N-PSDB; ADJ67708.
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13-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-MAR-1999;
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immunoglobulin variable region; immune cell protein; CD40;
phosphorylation-regulated cell signal transducer; TEM-1 beta-lactamase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli TEM-1 beta-lactamase.
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99US-0135926P.
2000US-0175968P.
2000US-00526106.
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Best Local Similarity 100.
Matches 181; Conservative
                                                                            Molecular chimaera for gene or virus directed enzyme prodrug therapy useful for treatment of cancer, viral infection or inflammation.
                                                                                                                                                                                                                                                                                                                                                           Gene directed enzyme prodrug therapy; GDEPT; virus directed enzyme prodrug therapy; VDEPT; beta-lactamase; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  efficiently detects multiple interaction between extracellular and intracellular protein with high throughput format. This is the amino aci sequence of antibiotic resistance enzyme TEM-1 beta-lactamase that can bused as a selectable gene in the fragment complementation system of the
                                                                                                                                                                                           20-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW16634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW16634 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 263 AA;
                                                                                                                                                                                                                19-NOV-1996;
                                                                                                                                                                                                                                      29-MAY-1997
                                                                                                                                                                                                                                                            WO9719180-A2
                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                              Escherichia
                                                                                                                                                                                                                                                                                                                                                                                              Beta-lactamase (including signal peptide).
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                                                                                                                                                                   (GLAX ) GLAXO
                                                                                                              1997-298117/27.
DB; AAT66736.
                                                                                                                                                                                                                                                                                                                                                   s directed enzyme inflammation.
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                                                                                                                                             Moore JT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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                                                                                                                                                                                                                                                                                                                              coli
                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry
                                                                                                                                                                   GROUP LTD
                                                                                                                                                                                         95GB-00023703.
                                                                                                                                                                                                                96WO-GB002845.
                                                                                                                                                                                                                                                                             1. .23
/label= Sig_peptide
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                              Ohmstede
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 925; DB 8;
Pred. No. 2.9e-94;
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Escherichia coli beta-lactamase (AAW16634), including the signal peptide,

Page

28;

38pp; English

is the expression product of a molecular chimaera, designated (AAT66737), in which the beta-lactamase gene is under control intermediate/early promoter. Vectors consisting of a transcri

under control of the CMV of a transcriptional

i pCMV-BL

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RESULT 5
AAW18680
ID AAW1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enzyme prodrug therapy. Expression of the beta-lactamase gene can be used for cell allows conversion of a prodrug into an agent toxic to the cell for treatment of cancer, viral (e.g. HIV) infection or inflammation.

Secretion of the enzyme has the advantage of increasing neighbouring cel kill
                                 The intracellular form (AAM18680) of TEM beta-lactamase is expressed pCMV-delBL (AAM70311) in which a PCR-amplified beta-lactamase coding sequence, minus the signal sequence, is placed under control of the intermediate/early promoter of cytomegalovirus. Intracellular beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prodrug therapy; gene directed virus directed enzyme prodrug t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                    expression
                                                                                                                                                   DNA construct for gene-directed enzyme prodrug therapy of lung cancer comprises lung- or neuroendocrine-specific promoter controlling
                                                                                                                                                                                                                                                                                             20-NOV-1995;
                                                                                                                                                                                                                                                                                                                         19-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                   29-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                               WO9719183-A2
                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                        beta-lactamase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW18680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW18680 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Intracellularly-expressed
                                                                                                                                                                                                                                                                 (GLAX ) GLAXO
                       .actamase constructs,
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ilarity 100.0%;
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                                                                                                                                    prodrug-converting
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ; gene directed enzyme prodrug therapy; GDEPT;
enzyme prodrug therapy; VDEPT; lung cancer;
pCMV-delBL.
        protein or neuroendocrine
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                       placed under control of promoter/enhancer elements
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              beta-lactamase
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Pred. No. 2.9e-94;
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                                                                                                                                      enzyme
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        genes,
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The expression constructs pRNH127 and pRNH155 contain identical sequences but were constructed using different strategies (see AAQ36498). The constructs comprise exons 2-7 of human CYP1A1 gene under the control of the inducible mouse metallothionein (MMT-1) promoter. The constructs also contain an open reading frame in the opposite orientation to the cytochrome P450 exons. This ORF encodes ampicillin resistance. The constructs are suitable for transformation of human fibroblasts derived from the xeroderma pigmentosum group A. Cultures of the transformed fibroblasts can be used to test substances for mutagenicity. The presence
                                                                                                                                                         gene
                                                                                                                                                                   In vitro method for testing mutagenicity of a chemical - by metachemical cell line consisting of transformed fibroblasts having detectable cytochrome P450 mixed function oxidase activity and o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer
                                                                                                                               Disclosure; Col 21-24; 24pp; English.
                                                                                                                                                                                                                                                           States JC,
                                                                                                                                                                                                                                                                                                               27-JUN-1991;
                                                                                                                                                                                                                                                                                                                                      27-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                          US5180666-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          xenobiotics;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYPIA1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ampicillin resistance protein
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04-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR31575;
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                                                                                                                                                         damage
                                                                                                                                                                                                                       1993-052845/06.
DB; AAQ36498.
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.9e-94;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 181;
A secretory beta-lactamase (AAR97619) is expressed from DNA construct pCMV-BI (AAT99220), in which the beta-lactamase coding sequence is under the control of the intermediate/early cytomegalovirus promoter. Beta-lactamase delivery to mammalian cells confers sensitivity to cephalosporin prodrugs. Liposomal DNA/5-fluorouracil prodrug combinations resulted in s.c. tumour regression in mice bearing A549 tumours. Survival of mice bearing human large cell lung H460 intrathoracic (i.t.) tumours was increased upon i.t. injection of the secretory beta-lactamase DNA
                                                                                                                                                      Molecular chimaera for use in enzyme gene therapy - is activated in target cell to express a secretable enzyme which cleaves a prodrug outside the cell into a cytotoxic or cytostatic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene therapy; gene directed enzyme prodrug therapy; GDEPT; virus directed enzyme prodrug therapy; VDEPT; prodrug activation; cytotoxic; cytostatic; cancer; tumour; retrovirus; vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the inducible cytochrome P450 gene allows metabolism of the substance to mutagenic metabolites. (Updated on 10-MAR-2003 to add missing OS field.)
                                                                                                                               Example 3; Page 57-58; 73pp; English
                                                                                                                                                                                                                                                                                                                18-NOV-1994;
                                                                                                                                                                                                                                                                                                                                            20-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                    WO9616179-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                          beta-lactamase; cephalosporin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Secretory beta-lactamase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-AUG-1996
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                                                                                                                                                                                                                                                                                      (WELL ) WELLCOME FOUND LTD.
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Pred. No. 3.3e-94;
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Best Local Simi
Matches 181;
cytochrome P450IA1 (CYPIA1) expression construct. Two clones, pRNH127 and pRNH15, were isolated by different methods and which both had the same sequence. The CYPIA1 construct is used in assays to test for cytotoxicity of humans to a chemical. The method comprises exposing human fibroblast cells normally not including any cytochrome P450 activity to potentially coxic chemicals. The cells having been transformed to express cytochrome P450, under the control of a controllable promoter through the CYPIA1 gene, upon exposure to the chemical in vitro. The chemical is metabolised intracellularly into a cytochrome metabolite by oxidation within the
                                                                                                                                                                                                                                The present sequence is encoded by a chimeric mouse metallothionein-cytochrome P450IA1 (CYP1A1) expression construct. Two clones, pRNH12
                                                                                                                                                                                                                                                                                                                                                                 Testing chemicals for cytotoxicity to human by detecting gene damage using recombinant fibroblasts transformed with cytochrome P450 gene control of inducible promoter.
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09-DEC-1992;
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(first entry)
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92US-00990295.
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Pred. No. 3.3e-94;
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             Escherichia coli beta-lactamase (AAM16635), lacking the signal peptide, is the expression product of a molecular chimaera, designated pCMV-delBL (AAT66738), in which the beta-lactamase gene is under control of the CMV intermediate/early promoter. Vectors consisting of a transcriptional regulatory DNA sequence linked to a beta-lactamase gene can be used for enzyme prodrug therapy. Intracellular expression of the beta-lactamase in a targetted cell allows conversion of a prodrug into an agent toxic to the cell for treatment of cancer, viral (e.g. HIV) infection or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fibroblasts through the intracellular cytochrome P450 mixed function oxidase enyzmes expressed by the cells. Gene damage in the test cells detected as an indication of cytotoxicity of the chemical. (Updated -MAR-2003 to correct PF field.)
                                                                                                                                              Molecular chimaera for gene or virus directed enuseful for treatment of cancer, viral infection
                                                                                                                                                                                                                                                                   20-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli
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Pred. No. 3.3e-94
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; VDEPT; beta-lactamase;
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                                                                                                                                               enzyme prodrug therapy on or inflammation.
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(Updated on 25
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                   The secreted form (AAW18679) of TEM beta-lactamase is expressed by pCMV-BL (AAT70309) in which a PCR-amplified beta-lactamase coding sequence is placed under control of the intermediate/early promoter of cytomegalovirus. Secretory beta-lactamase constructs, placed under control of promoter/enhancer elements of lung- associated protein or
                                                                                                                                                                                                                             DNA construct for gene-directed enzyme prodrug therapy of lung cancer comprises lung- or neuroendocrine-specific promoter controlling
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                                                                                                                                                               Example 8ii;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-NOV-1995;
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                                                                                                                                                                                                             prodrug-converting
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/label= Mat_protein
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bred. No. 3.3e-94;
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This invention describes a novel tetracycline assay that uses recombinant prokaryotic cells comprising a luciferase gene under the transcriptional control of a tetracycline repressor and tetracycline promoter and involves the detection of luminescence emitted form the cells. The assay can be used to distinguish tetracycline form other microbial agents. The invention also describes a novel plasmid comprising either the luxCDABE genes, a tetracycline repressor (TetR) and comprising either the luxCDABE from Tn10, or the insect luciferase gene, a tetracycline repressor (tetR) and a tetracycline promoter (TetA) from Tn10. The tetracycline assay method can be used for the determination of tetracycline in a sample,
                                                                                                                                                                                                                                                                                                      14-NOV-1997;
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                                                                                                                                        Disclosure; Page 47-48; 67pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            insect;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Tn10;
                                                                                                                                                                                                                                                     KURITTU J.
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Pred. No. 3.3e-94;
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 181;
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                                                                                                                Selecting monoclonal antibodies,
                                                                                                                                       N-PSDB;
                                                                                                                                                                        Breitling
                                                                                                                                                                                                                      11-JAN-1999;
                                                                                                                                                                                                                                             11-JAN-1999;
                                                                                                                                                                                                                                                                     13-JUL-2000
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                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                    Expression vector; antibody
                                                                                                                                                                                                                                                                                                                                                                           Expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB10442 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 286 AA;
                                                                                          antibody
                                                                                                      hybridomas attached to
                                                                                                                                                                                                (DEKR-)
                                                                                                                                                                                                                                                                                                                                        lymphocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                  2000-499832/45.
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                                                                                                                                        AAA71430.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HPETLVKVKDAEDQLGARVGY1ELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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                                                                                                                                                                         Poustka
                                                                                                                                                                                                                                                                                                                                        myeloma cell;
                                                                                                                                                                                                                       99DE-01000635
                                                                                                                                                                                                                                               99DE-01000635
                                                                                                                                                                                                                                                                                                                                                                           pSEX15G2
                                                                                                                                                                                                                                                                                                                                                                                                 entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                         ۶
                                                                                                    antibody-binding
                                                                                                                                                                         Moldenhauer
                                                                                                                                                                                                                                                                                                                                                                           bla protein.
                                                                                                                                                                                                                                                                                                                                        binding protein; monoclonal antibody; Neo-R; hybridoma; protein G; bla protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 925; DB 2;
Pred. No. 3.3e-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ⋛
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                    by expressing them on the surface binding protein, then reaction with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 286;
                                                                                                                                                                                                                                                                                                                                      bla protein.
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This invention describes a novel method for the selection of monoclonal antibodies (MAb) which comprises (i) fusing B lymphocytes with myeloma cells to produce antibody-producing hybridomas such that the antibodies are presented at the surface of the hybridomas by an antibody-binding protein (I); and (ii) binding the antibody to antigens (Ag). The

Claim 16;

Fig 3;

22pp; German

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ARBSULT 13
AAB10438
ID AAB10
XX AAB10
XX AAB10
XX O1-DE
XX Expre
XX Expre
XX Expre
XX Synth
XX I1-JA
XX 11-JA
XX 11-JA
XX I1-JA
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X
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention also describes antibody-binding proteins (I) that comprise a combination of the signal peptide of a murine immunoglobulin (Ig) kappa chain or a murine MHC (major histocompatibility complex) Class I k(k) molecule, an antibody-binding site of proteins A, G, L or LG, and the transmembrane domain of PDGFR (platelet-derived growth factor receptor) or CD52. The method is used to select MAb with specificity for particular antigens. MAb can be selected without separate culture of hybridomas, and selection can be made against many antigens in a library, optionally on the basis of strength of affinity for a particular antigen. Complex mixtures of hybridomas can be used for selection, reducing the time and cost involved in MAb selection. This sequence represents the bla protein protein contained in the expression vector pSEXISG2 which contains the bla protein for selection, Neo-R and protein G described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 286 AA;
                                                                                                                   antibody library.
                                                                                                                                                     Selecting monoclonal antibodies, by expressing them on the surface of hybridomas attached to antibody-binding protein, then reaction with
                                                                                                                                                                                                                                                                         N-PSDB; AAA71428.
                                                                                                                                                                                                                                                                                                           WPI; 2000-499832/45.
                                                                                                                                                                                                                                                                                                                                                                                 Breitling F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-JUL-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DE19900635-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Expression vector; antibody binding protein; monoclonal antibody; Neo-R; B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB10438 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DEKR-) DEUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              KREBSFORSCHUNGSZENTRUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                 Poustka A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99DE-01000635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99DE-01000635
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                                                                                                                                                                                                                                                                                                                                                                                     Moldenhauer
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Pred. No. 3.3e-94;
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Claim 16; Fig 1; 22pp;

Selecting monoclonal antibodies, by expressing them on the surface

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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC This invention describes a novel method for the selection of monoclonal CC antibodies (MAb) which comprises (i) fusing B lymphocytes with myeloma CC cells to produce antibody-producing hybridomas such that the antibodies CC are presented at the surface of the hybridomas by an antibody-binding CC protein (I); and (ii) binding the antibody to antigens (Ag). The CC invention also describes antibody-binding proteins (I) that comprise a CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa CC chain or a murine MHC (major histocompatibility complex) Class I k(k) CC molecule; an antibody-binding site of proteins A, G, L or LG, and the CC transmembrane domain of PDGFR (platelet-derived growth factor receptor) CC or CD52. The method is used to select MAb with specificity for particular antigens. MAb can be selected without separate culture of hybridomas, and CC election can be made against many antigens in a library, optionally on CC the basis of strength of affinity for a particular antigen. Complex CC mixtures of hybridomas can be used for selection, reducing the time and CC cost involved in MAb selection. This sequence represents the Neo-R CC protein contained in the expression vector pSEXIII4 which contains the CC bla protein, Neo-R and protein G described in the method of the invention
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                                  WPI; 2000-499832/45.
N-PSDB; AAA71429.
                                                                                    Breitling
                                                                                                                                                          11-JAN-1999;
                                                                                                                                                                                          11-JAN-1999;
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                                                                                                                                                                                                                                                                DE19900635-A1
                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                              Expression vector; antibody binding protein; monoclonal antibody; Neo-R; B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.
                                                                                                                                                                                                                                                                                                                                                                                    Expression vector pSEX11G2 bla protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB10440;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60
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                                                                                       Moldenhauer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC This invention describes a novel method for the selection of monoclonal CC antibodies (MAb) which comprises (i) fusing B Jymphocytes with myeloma CC cells to produce antibody-producing hybridomas such that the antibodies CC are presented at the surface of the hybridomas by an antibody-binding CC protein (I); and (ii) binding the antibody antipody binding proteins (Ag). The CC invention also describes antibody-binding proteins (I) that comprise a CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa CC chain or a murine MHC (major histocompatibility complex) Class I k(k) CC molecule; an antibody-binding site of proteins A, G, L or LG, and the CC transmembrane domain of PDGFR (plattelet-derived growth factor receptor) CC or CD52. The method is used to select MAb with specificity for particular CC contigens. MAb can be selected without separate culture of hybridomas, and CC the basis of strength of affinity for a particular antigen. Complex CC mixtures of hybridomas can be used for selection, reducing the time and CC cost involved in MAb selection. This sequence represents the bla protein CC bla protein, Neo-R and protein G described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                   bla resistance marker; recombinant host cell; saccharification; fermentation; polysaccharase; oligosaccharide degradation; celZ gene; glucanase; integration vector; pLO12306.
                                                                                                                                     30-NOV-2000
                                                                                                                                                                                                                                                                                                                              Protein encoded by bla resistance marker of integration vector pLO12306.
                                                                                                                                                                                                                                                                                                                                                                      20-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB50898 standard; protein; 286 AA
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                                                        26-MAY-1999;
                                                                                             26-MAY-2000;
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                    (UYFL ) UNIV FLORIDA RES FOUND
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Pred. No. 3.3e-94;
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Best Local Similarity
Matches 181; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polymucleotide encoding a polymaccharase under the transcriptional control of a surrogate promoter capable of increasing expression of the polymaccharase. The host cell also contains a second heterologous polymucleotide encoding a secretory polypeptide to facilitate the secretion of the expressed polysaccharase. The recombinant host cell is useful for producing polysaccharase which is useful for enzymatically degrading oligosaccharides such as lignocellulose, hemicellulose, cellulose, pectin or their combinations, and fermenting the product to ethanol, by simultaneous saccharification and fermentation processes. The present sequence is encoded by an integration vector which was introduced into cells to generate recombinant host cells. The vector contains a surrogate promoter from Zymomonas mobilis, the celZ gene from Erwinia chrysanthemi, resistance markers bla and tet, and Klebsiella oxytoca
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 286 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant host cells useful for producing polysaccharase for degrading oligosaccharides, comprises a first heterologous polynucleotide encoding polysaccharase under control of surrogate promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 82-83; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is given in a specification relating to a recombinant host cell suitable for simultaneous saccharification fermentation. The host cell contains at least one heterologous
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                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 925; DB 4; Length 286; ilarity 100.0%; Pred. No. 3.3e-94; Conservative 0; Mismatches 0; Indels
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Search completed: June 10, 2005, 10:49:10 Job time: 71.1783 secs

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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

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US-09-919-901-7
US-09-919-901-7
US-09-919-901-21
US-09-490-070A-265
US-09-490-070A-365
US-09-490-153-362
US-09-490-153-362
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APPLICANT: States, J. Christopher
APPLICANT: Hines, Ronald N.
APPLICANT: No. 5525482ak, Raymond F.
APPLICANT: No. 5525482ak, Raymond F.
TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (313) 689-4071
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (313) 689-3554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Reising, Ethington, Barnard, Perry & Milton STREET: P.O. Box 4390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELECUPALICE (313)
                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Kohn, Kenneth I. REGISTRATION NUMBER: 30, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/339,658 FILING DATE: 15-NOV-1994 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Troy
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                       KELTAFIHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 180
                                                                              AGQEQLGRRIHYSQNDLVEYSFVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGF 143
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                                                                                                                                                                                                                                         100.0%; Score 925; DB 1; I larity 100.0%; Pred. No. 4.1e-100; Conservative 0; Mismatches 0;
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; SEQ ID NO 7;
LENGTH: 286;
; TYPE: PRT;
; ORGANISM: Artificial Sequence
US-09-263-933-7
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; ORGANISM: Artificial Sequence US-09-263-933-14
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                                                                                     SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/09263933 Patent No. 6280940
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Best Local Similarity
Matches 181; Conserv
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                                                                                                                          TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER: 05 EQ ID NOS: 33
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CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
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APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
                                           TYPE: PRT
                                                                  CENGTH:
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Query Match

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APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
APPLICANT: PATICH, AMY K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 286
                                                    Sequence 265, Application US/09025769B Patent No. 6300064
GENERAL INFORMATION:
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Best Local (
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ORGANISM: Artificial Sequence
-09-263-933-21
                    APPLICANT:
APPLICANT:
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RESULT 7
US-09-025-769B-362
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INFORMATION FOR SEQ ID NO: 26
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                               Sequence 362, Application US/09025769B Patent No. 6300064
GENERAL INFORMATION:
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Best Local Similarity
                APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
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REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MO
TELECOMMUNICATION INFORMATION:
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APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
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APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
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NUMBER OF SEQUENCES: 3
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
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(212)596-9090
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ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas

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US-09-919-901-7
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
                                                   FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
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INFORMATION FOR SEQ ID NO: 30
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SOFTWARE: PatentIn Ver.
SEQ ID NO 7
                                                                                                                                                                                           APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Pattck, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USB IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
                                    NUMBER OF SEQ ID NOS: 33
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STREET: New York
CITY: New York
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CURRENT APPLICATION DATA:
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TOPOLOGY: linear
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Local Similarity 100.0%;
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Pred. No. 4.1e-100;
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; OTHER INFORMATION: US-09-919-901-7
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APPLICANT: Potts, Karen E.
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Patent No. 6599738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 14
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Best Local Similarity
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APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR FILING DATE: 1999-02-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
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144 KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ
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100.0%; Pred. No. 4.1e-100;
tive 0; Mismatches 0;
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RESULT 11
US-09-490-070A-265
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US-09-919-901-21
                                                                                                                                                                                                                                                                                                                                                               Sequence 265, Application US/09490070A Patent No. 6696248
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 925; DB 4; 1
Best Local Similarity 100.0%; Pred. No. 4.1e-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 21
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Patent No. 659973
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CURRENT FILLING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION:
                                                                                                                                                         Moroney, Šimon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

MUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Knappik, Achim
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                                                                CITY: Washington STATE: D.C.
                                                                                                    STREET: 1666 K Street, N.W., Suite
                                        COUNTRY: USA
                                                                                                                          ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/09919901
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Ilag, Vic
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GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEPAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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APPLICATION NOMBER: US/09/490,070A

FILING DATE: 24-Jan-2000

PRIOR APPLICATION UNMBER: BP 95 11 3021.0

PRIOR APPLICATION NUMBER: BP 95 11 3021.0

PRIOR APPLICATION NUMBER: BP 95 11 3021.0

PRIOR DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Colin G. Sandercock, Esq.

REGISTRATION NUMBER: 31,298
               ZIP: 20006
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER: DOS
                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Protein/(Poly)peptide libraries NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 265:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Knappik, Achim
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TYPE: amino acid
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SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
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Plueckthun, Andreas
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Ilag, Vic
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Pred. No. 4.1e-100;
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CURRENT APPLICATION DATA:

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RESULT 13
US-09-490-153-265
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; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 362:
US-09-490-070A-362
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Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
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FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
RECISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Protein/(Poly)peptide libraries NUMBER OF SEQUENCES: 373
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                                                                                                                                                                                                                                                                                    CITY: New York
STATE: New York
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                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 10021
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                                                                                                                                                                                                                                                                                                                                  STREET:
APPLICATION NUMBER: US/09/025,7698
                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                              Moroney, Simon
Plueckthun, Andreas
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Ilag, Vic
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I LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-490-153-265
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US-09-490-153-362
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GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)

CURRENT APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATE: US/09/490,153

FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
RILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
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Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
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REGISTRATION NUMBER: 27,794
REPERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEPAX: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq.
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
COUNTRY: USA
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Pred. No. 4.1e-100;
Mismatches 0;
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APPLICANT: FOLCE, AGAIN.

APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/10/191,966

CURRENT APPLICATION NUMBER: US/09/263,933

PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 7

LENGTH: 286

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

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; TYPE: amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 362:
US-09-490-153-362
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Patent No. 6790612
GENERAL INFORMATION:
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Best Local Similarity
Matches 181; Conserv
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INFORMATION FOR SEQ ID NO: 362:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                           OTHER INFORMATION: :
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REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
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61 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
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                                                    HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 83
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Result
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            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2005 Compugen
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beta-lactamase (EC Bla probein - Salm beta-lactamase (EC beta-lactamas
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T51301
Deta-lactamase (EC 3.5.2.6) - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C;Accession: T51301
        A; Reference number: S47060
A; Accession: S47061
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	45	44	43	42	41	40	9	38	37	36	3 5	34	ω G	32	31 ·	30
291 2 542075 306 2 665674 311 2 JN0520 305 2 A65156 305 2 A65080 305 2 A65080 306 2 S47330 291 2 JP0074 310 2 JL0091 310 2 JL0091 305 1 C45822 263 2 S23929 288 2 JQ1136 294 2 S44080 311 1 S02714 304 2 A45501	350.5	350.5	353.5	354	354.5	354.5	356.5	357	359.5	67	368	368	368	371.5	372.5	377.5
2 S42075 2 G69674 2 JN0520 2 A61156 2 A57002 2 A60680 2 JP0074 2 JF0074 2 JL0091 1 C45822 1 C45822 2 S23929 2 JQ1156 2 S44080 1 S02714 2 A49789 2 A35001	37.9	37.9	38.2	38.3	38.3	38.3	38.5	38.6	38.9	39.7	39.8	39.8	39.8	40.2	40.3	40.8
542075 G69674 JN0520 A61156 A51002 A60680 547330 JP0074 JL0091 JL0091 JC45822 S23929 JC1136 S44080 S44080 S44080 S44080 S44080 S02714 A49789	304	304	311	294	288	263	305	310	291	306	305	305	305	311	306	291
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beta-lactamase	A35001	A49789	S02714	S44080	JQ1136	S23929	C45822	JL0091	JP0074	S47330	A60680	A57002	A61156	JN0520	G69674	S42075

ALIGNMENTS

	C;Accession: T51301 R;WACH, A.; BRACHAT, A.; ALBERTISEGUI, C.; REBISCHUNG, C.; PHILIPPSEN, P. Yeast 13, 1065-1075, 1997 A;Title: Heterologous HIS3 marker and GFP reporter modules for PCR-targeting in Saccharon A;Reference number: Z09587
	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-286 <wac> A;Cross references: EMBL:AJ002683; PIDN:CAA05686.1 C;Genetics: A;Gene: bla C;Superfamily: beta-lactamase I C;Keywords: hydrolase</wac>
-	Query Match 100.0%; Score 925; DB 2; Length 286; Best Local Similarity 100.0%; Pred. No. 2.5e-76; Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
· · · · · · · · · · · · · · · · · · ·	QY 1 HPETLYKVKDAEDQLGARVGY1ELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60
	QY 61 AGQEQLGRRIHYSQNDLVEYSEVTEKHLTDGWTVRELCSAAITMSDNTAANLLLTTIGGP 120
	QY 121 KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 180
	Oy 181 Q 181 Db 204 Q 204
	RESULT 2 \$47061 , \$47061 , beta-lactamase (BC 3.5.2.6) - phage phi-X174 C;Species: phage phi-X174 C;Species: phage phi-X174 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004 C;Accession: \$47061 R;Henrich, B.; Schmidtberger, B. submitted to the EMBL Data Library, July 1994 A;Description: A variant of phiX174 gene B-based positive selection vectors with enhanced a.Reference number: 427060

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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-286 <HEN>
A;Cross-references: UNIPROT:Q38058; EMBL:Z35638; NID:g520996; PIDN:CAA84692.1; PID:g5209
C;Superfamily: beta-lactamase I
C;Keywords: hydrolase
beta-lactamase (EC 3.5.2.6) precursor - Escherichia coli plasmids N;Alternate names: beta-lactamase TEM-6 (for blaT-6 DNA); penicil C;Species: Escherichia coli C;Date: 30-Nov-1980 #sequence revision 01-Sen-1981 #+ev+ ch-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X76682; NID:g453622; PIDN:CAA54104.1; PID:g453623 A;Note: submitted to the EMBL Data Library, December 1993 C;Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene 148, 67-70, 1994
A;Title: Universal beta-galactosidase cloning vectors for promoter A;Reference number: A57991; MUID:95011660; PMID:7926839
A;Accession: S41975
A;Status: not compared with conceptual translation
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Pred. No. 2.5e-76;
Mismatches 0;
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Pred. No. 2.5e-76;
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01-Sep-1981 #text_change 16-Aug-2004
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C;Keywords: antibiotic resistance; hydrolase; membrane protein F;1-23/Domain: signal sequence #status predicted <SIG>F;24-286/Product: beta-lactamase #status experimental <MAT>F;68/Active site: Ser #status predicted F;75-121/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 24-35,'K', 38-286 <AMB>
A;Residues: 24-35,'K', 38-286 <AMB>
A;Experimental source: plasmid R6K
R;Kornacki, J.A.; Burlage, R.S.; Figurski, D.H.
J. Bacteriol. 172, 3040-3050, 1990
A;Title: The kil-kor regulon of broad-host-range plasmid RK2: nucleotide sequence,
A;Reference number: A35387; MUID:90264294; PMID:2160936
A;Accession: A35387
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R;Ambler, R.P.; Scott, G.K.
Proc. Natl. Acad. Sci. U.S.A. 75, 3732-3736, 1978
A;Title: Partial amino acid sequence of penicillinase coded by Escherichia coli plasmid A;Reference number: A93820; MUID:79012483; PMID:358199
A;Accession: A93820
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Proc. Natl. Acad. Sci. U.S.A. 75, 3737-3741, 1978
A;Title: Nucleotide sequence of the ampicillin resistance gene of Escherichia coli plasmi A;Reference number: A93821; MUID:79012484; PMID:358200
A;Accession: A93821
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Cold Spring Harb. Symp. Quant. Biol. 43, 77-90, 1979
A;Title: Complete nucleotide sequence of the Escherichia
A;Reference number: A90923; MUID:80002802; PMID:383387
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A;Cross-references: EMBL:X57972; NID:g41816; PIDN:CAA41038.1;
A;Experimental source: ISI-like blaT-6 DNA
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A; Residues: 182-286 < KOR>
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Pred. No. 7.2e-76;
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A; Gene: bla(TEM-3)
A; Genome: plasmid
C; Superfamily: beta
C; Keywords: antibio
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Mol. Gen. Genet. 235, 113-121, 1992
A;Title: A new example of physical linkage between Tn1 and Tn21: the antibiotic multiple A;Reference number: S30112; MUID:93062798; PMID:1331747
A;Accession: S30113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            beta-lactamase (EC 3.5.2.6) TEM-3 - Klebsiella pneumoniae plasmid pCFF04 C;Species: Klebsiella pneumoniae C;Pate: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004 C;Accession: S30113
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Plasmid 29, 241-244, 1993
A;Title: Development of a native plasmid as a cloning vector A;Reference number: I40904; MUID:93361581; PMID:7889234
A;Accession: I40905
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A;Note: cloning vector pCG1408 engineered and expressed in Clavibacter xyli subsp.
C;Date: 15-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Oct-2000
C;Accession: I40905
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A;Residues: 1-286 <RES>
A;Cross-references: EMBL:U21228; NID:g885956; PIDN:AAA70411.1; PID:g885958
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A; Residues: 1-286 < MAB>
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                                                                                                                                                                                                                                                                                       ;Genome: plasmid
;Superfamily: beta-lactamase I
;Keywords: antibiotic resistand
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                                                                                                                          HPETLVKVKDAEDKLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRVD
                                                                                                                                           HPETLVKVKDAEDQLGARVGYIELDLNSGKILESPRPEERPPMMSTPKVLLCGAVLSRID
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  KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 180
                                                                AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                        AGQEQLGRRIHYSQNDLVKYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 143
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llarity 97.8%;
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Pred. No. 7.2e-76;
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C;Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 22-Jun-1999 C;Accession: S60310
C;Accession: S60310
R;Chanal, C; Poupart, M.C.; Sirot, D.; Labia, R.; Sirot, J.; Cluzel, R. Antimicrob. Agents Chemother. 36, 1817-1820, 1992
A;Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase gene A;Reference number: S60310; MUID:93037315; PMID:1416873
A;Accession: S60310
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A;Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes. A;Reference number: S60310; MUID:93037315; PMID:1416873
A;Accession: S60312
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                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X65252; NID:g296951; PIDN:CAA46344.1; PID:g296952 C;Superfamily: beta-lactamase I
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A; Residues: 1-286 < CHA>
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A;Cross-references: EMB
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176; Conserv
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AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
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97.2%;
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                                                                                                                                                                               Score 906; DB 2; 1
Pred. No. 1.3e-74;
3; Mismatches 2;
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Pred. No. 1.1e-74;
3; Mismatches 2
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Bla protein - Salmonella typhimurium plasmid NTP16
NyAlternate names: beta lactamase homolog
CySpecies: Salmonella typhimurium
CyDate: 30-Sep-1993 #sequence_revision 30-Sep-1993
CyAccession: JQ1546
R;Cannon, P.M.; Strike, P.
Plasmid 27, 220-230, 1992
A;Title: Complete nucleotide sequence and gene organ
        A;Reference number: JQ1538; MUID:92383313; PMID:1325061 A;Accession: JQ1546
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C;Date: 12-Apr-1996 #sequence revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: S60311; B737392; PQ0498
R;Chanal, C.; Poupart, M.C.; Sirot, D.; Labia, R.; Sirot, J.; Cluzel, R.
Antimicrob. Agents Chemother. 36, 1817-1820, 1992
A;Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase gen/A;Reference number: S60310; MUID:93037315; PMID:1416873
A;Accession: S60311
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S60311
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Plasmid 24, 218-226, 1990
Plasmid 24, 218-226, 1990
A;Title: Sequencing and expression of aadA, bla, and tnpR from A;Reference number: A37392; MUID:91172904; PMID:1963948
A;Accession: F37392
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A; Residues: 1-32 < TOL>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGQEQLGRRIHYSQNDLVKYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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97.2%;
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Pred. No. 1.3e-74;
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A;ACCEBBALO....A;ANOIECULE type: DNA
A;Residues: 1-30,'L',32-286 <LEE>
A;Cross references: GB:K62115; NID:g48988; PIDN:CAA44025.1;
A;Cross references: plasmid BWH77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Lee, K.Y.; Hopkins, J.D.; Syvanen, M.
J. Bacteriol. 172, 3229-3236, 1990
A;Title: Direct involvement of IS26 in an antibiotic resistance A;Reference number: A35395, MUID:90264317, PMID:2160941
A;Accession: A35395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Date: 21-Nov-1993 #sequence revision 10-Nov-1995 #text_change 15-Oct-C;Accession: S16146; A35395; S18767 G;Accession: S16146; A35395; S18767 R;Podbielski, A.; Schoenling, J.; Melzer, B.; Warnatz, K.; Leusch, H.G. J. Gen, Microbiol. 137, S69-578, 1991 A;Title: Molecular characterization of a new plasmid-encoded SHV-type b A;Reference number: S16146; MUID:91237320; PMID:2033379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             beta-lactamase (EC 3.5.2.6) 2A precursor - N;Alternate names: beta-lactamase SHV2A C;Species: Klebsiella pneumoniae
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S16146
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A;Residues: 1-286 <CANS
A;Cross-references: UNIPROT:Q8L2F9
C;Genetics:
A;Genome: plasmid
C;Superfamily: beta-lactamase I
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C;Superfamily: beta-lactamase
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A;Experimental source: plasmid pZMP1
R;Lee, K.Y.; Hopkins, J.D.; Syvanen, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type:
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                                                                GQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGFX 121
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  ELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQQ 181
                                          GDEQLERKIHYRQQDLVDYSPVSEKHLADGMTVGELCAAAITMSDNSAANLLLATVGGPA 142
                                                                                                                                             PETIVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRIDA 61
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67.8%; Pred. No. 1.7e-50;
tive 26; Mismatches 32
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Pred. No. 1.3e-74;
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C;Species: Escherichia coli
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1993
C;Accession: S00464
R;Barthelemy, M: Peduzzi, J.; Labia, R.
Biochem. J. 251, 73-79, 1988
Biochem. J. 251, 73-79, 1988
A;Title: Complete amino acid sequence of p453-plasmid-mediated PIT-2 beta-lactamase A;Reference number: $00464; MUID:88268817; PMID:3260490
A;Accession: $00464
A;Molecule type: protein
A;Residues: 1-265 <BAR>
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         beta-lactamase (EC 3.5.2.6) class A - Escherichia coli plasmid p453
N;Alternate names: beta-lactamase PIT-2; beta-lactamase SHV-1
C;Species: Escherichia coli
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1993
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A;Title: Nucleotide sequence of SHV-2 beta-lactamase gene. A;Reference number: A60679; MUID:90351141; PMID:2201259
A;Accession: A60679
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                                                                                                                                                                                                                              ;Genome: plasmid
;Superfamily: beta-lactamase I
;Keywords: antibiotic resistance; hydrolase
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;Superfamily: Beta-lactamase I
;Keywords: antibiotic resistance; hydrolase
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                       GQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGFK 121
                                                                                                     PETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFFMMSTFKVLLCGAVLSRIDA
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   GDEQLERKIHYRQQDLVDYSPVSEKHLADGMTVGELCAAAITMSDNSAANLLLTAVGGPA
                                                                             PQPLEQIKLSESQLSGRVGMIEMDLASGRTLTAWRADERFPMMSTFKVVLCGAVLARVDA
                                                                                                                                                       Conservative
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                                                                                                                                                                     68.8%;
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                                                                                                                                                   Score 636; DB 2; I
Pred. No. 3.6e-50;
6; Mismatches 32;
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R;Huletsky, A.; Couture, F.; Levesque, R.C. Antimicrob. Agents Chemother. 34, 1725-1732, 1990 A;Title: Nucleotide sequence and phylogeny of SHV-2 beta-lactamase. A;Reference number: A44998; MUID:91136192; PMID:2285285 A;Accession: A44998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     beta-lactamase (EC 3.5.2.6) SHV-2 - Escherichia coli
C;Species: Escherichia coli
C;Date: 01-Dec-1999 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993
                                                                                                                                                                                 C; Superfamily: Beta-lactamase I C; Keywords: antibiotic resistan
                                                                                                                                                                                                                                                                                                                                                                                                             R;PodDielski, A.; Melzer, B.
Nucleic Acids Res. 18, 4916, 1990
Nucleic Acids Res. 18, 4916, 1990
A;Title: Nucleotide sequence of the gene encoding the SHV-2 beta-lactamase
A;Reference number: S12703; MUID:90370479; PMID:2395654
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A;Residues: 1-265 <BAR>
C;Superfamily: beta-lactamase I
C;Keywords: antibiotic resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Barthelemy, M.; Peduzzi, J.; Yaghlane, H.B.; Labia, R. FEBS Lett. 231, 217-220, 1988
A;Title: Single amino acid substitution between SHV-1 beta-lactamase and cefotaxime-hydro A;Reference number: S02434; MUID:88196385; PMID:3129309
A;Accession: S02434
                                                                                                                                                                                                                              A;Genome: plasmid
                                                                                                                                                                                                                                                               C; Genetics:
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C;Accession: A44998; S12703
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                                                                             68.8%; Score 636; DB 1;
67.8%; Pred. No. 4e-50;
tive 26; Mismatches 32
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Search Job ti	문	Ş	дb	Ş	ర్థ
Search completed: June 10, 2005, 10:58:45 Job time : 14.1993 secs	143 GLTAFLRQIGDNVTRLDRWETELNEALPGDARDTTTPASMAATLRKLLTSQRLSARSQRQ 202	122 ELTAFIHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQQ 181	83 GDEQLERKIHYRQQDLVDYSPVSEKHLADGMTVGELCAAAITMSDNSAANLLLATVGGPA 142	62 GQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGFK 121	23 PQPLEQIKLSESQLSGRVGMIEMDLASGRTLTAWRADERFPMMSTFKVVLCGAVLARVDA 82

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Result
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Q6WWY3
Q6WWY3
Q6WWY3
Q6W667
Q6KB67
Q38058
Q79CL6
Q7
       Q8KSD3
Q8VP43
Q8VP43
Q933Z8
Q93AD7
Q93AT7
Q93GT3
Q6A2S3
Q6LBN9
Q6LCV6
Q6TMH1
Q6UVM7
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Q6wwy5 klebsiella Q6wwy4 hafnia alve Q6wwy4 hafnia alve Q6wwy8 escherichia Q6wb67 hordeum vul Q38058 bacteriopha Q00626 staphylococ Q79c16 methylobaci Q79dr3 escherichia Q38212 bacteriopha Q6pru7 escherichia Q84449 klebsiella Q6pru6 acinetobact Q6qiv0 serratia ma Q6qiv0 serratia ma Q6qiv0 serratia ma Q6giv1 secherichia Q8462594 salmonalla Q53043 klebsiella Q8vp43 klebsiella Q8vp43 klebsiella Q8vp43 klebsiella Q8vp43 klebsiella Q8vp43 klebsiella Q83278 escherichia Q93477 escherichia Q93477 scherichia Q93477 scherichia Q50473 klebsiella Q61bn9 pseudomonas Q61br0 pseudomonas Q61br0 reisseria g06tmh1 streptococc Q6uvm7 acinetobact Q6wr7j4 escherichia
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70 escherichia	Q9r770	09R770	N	286	99.5	920	ഗ
82 klebsiella	Q9k582	Q9K582	N	286	99.5	920	4
x1 escherichi	Q9eyx1	Q9EYX1	N	286	99.5	920	w
85 escherichi	Q8ga85	Q8GA85	N	286	99.5	920	2
x1 klebsiel	Q844x1	Q844X1	N	286	99.5	. 920	_
	Q7dh	Q7DHD3	N	286	99.5	920	0
y3 salmonella	Q7dfy3	Q7DFY3	N	286	99.5	920	9
01	Q7br75	Q7BR75	N	286	99.5	920	œ
57 shigella	Q7bp5	Q7BP57	N	286	99.5	920	7
Φ	Q7b891	Q7B899	N	286	99.5	920	0
x5 citrobacter	Q7b3x5	Q7B3X5	N	286	99.5	920	տ
d4 acinetobac	Q6wzd4	Q6WZD4	N	286	99.5	920	4.
x2 zymomonas	Q6wrx2	Q6WRX2	N	286	99.5	920	w
jl enterobacte	Q6w9j1	Q6W9J1	N	286	99.5	920	N

ALIGNMENTS

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RESULT 2
Q6WWY4
ID Q6WW
AC Q6WW
DT 05-J
DT 05-J
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Best Local Similarity
Matches 181; Conserva
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
Beta-lactamase (Fragment).
Q6WWY4;
Q6WWY4;
05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
Submitted (APR-2004) to the EMBI/GenBank/DDBJ databases.
EMBI, AV265885, AAP93843.1;
HSSP; P00807; 1KGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klebsiella oxytoca.
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Klebsiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000871; Beta_lactamase_A.
PRINTS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE_A; 1.
NON TEP
                                                                                                                                                                                                                    121 KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ
                                                                                                                                                                                                                                                                                        AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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229 AA;
(TrEMBLrel. 27, (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                  PRELIMINARY;
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Best Local
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Q6WWY8;
Q6WWY8;
05-JUL-2004 (TrEMBLrel. 27, C
05-JUL-2004 (TrEMBLrel. 27, L
05-JUL-2004 (TrEMBLrel. 27, L
Beta-lactamase (Fragment).
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SEQUENCE
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PRINTS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE_A; 1.
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Obert C.A., Goldstone C.M.,
Submitted (APR-2004) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=blaTEM;
Klebsiella pneumoniae.
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HSSP; P00807; 1KGE.
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NCBI_TaxID=569;
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                                                                                                                                                              InterPro; IPR001466; Beta lactamase.
InterPro; IPR000871; Beta lactamase A.
Pfam; PF00144; Beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
                                                                                                                                                                                                                                                                                                                                                        STRAIN=MISC112;
                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Klebsiella.
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                                                                                                                                             PROSITE;
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                                                                                                                                        PS00146; BETA_LACTAMASE_A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q 181
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                                                                    241
241 AA;
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232 AA;
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                                                                 241
26407 MW;
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100.0%;
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                                                                                                                                                                                                                                                                                                            Gordon D.M., Riley M.A.;
EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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Score 925; DB 2;
Pred. No. 1.8e-71;
                                                                      38DF2AFDF0C5807D CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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InterPro; IPR000871; Beta_lactamase_A.
Pfam; PF00144; Beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
PROSTTE; PS00146; BETA_LACTAMASE_A; 1.
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Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
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Pred. No. 1.8e-71;
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01-NOV-1996
01-NOV-1996
01-JUN-2003
                                                                                 SEQUENCE FROM N.A.

MEDIJINE=95172401; PubMed=7867948; DOI=10.1016/0378-1119(94)00839-K;
Henrich B., Schmidtberger B.;
"A variant of phiX174 gene E-based positive selection vectors with enhanced lytic potential.";
Gene 154:51-54(1995).

EMBLI; 235638; CAR84692.1; -.

PIR; S47061, S47061.

HSSP; Q9R435; 1HTZ.

InterPro; IPR0010476; Beta_lactamase.

InterPro; IPR000871; Beta_lactamase_A.

Pfam; PF00144; Beta_lactamase; 1.

Procession of the p
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Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jansen C., Korell M., Eckey C., Biedenkopf D., Submitted (MAY-2004) to the EMBL/GenBank/DDBJ (EMBL, AJ71)7739; CAG30723.1; -. GAG30723.1; -. 
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Viruses; ssDNA viruses;
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PROSITE; PS00146; BETA_LACTAMASE_A;
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Plasmid.
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Q00626; O08022; O08102; O09393; O09396; O09397; O09398; O09399;
Q006400; O09401; O09402; O09403; O09404; O09405; O09406; O09407;
Q009408; O009481; O009482; O009490; Q57339;
Q1-NOV-1996 (TERMBLrel. 01, Created)
Q1-NOV-1996 (TERMBLrel. 01, Last sequence update)
Q5-OCT-2004 (TERMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Needham C., Noble W.C., Dyke K.G.;
"The staphylococcal insertion sequence IS257 is active.";
"Issaid 34:198-205(1995).
EMBL; U36912; AAB39957.1; -.
EMBL; U36911; AAB39956.1; -.
InterPro; IPR001466; Beta lactamase.
InterPro; IPR00147; Beta lactamase A.
Pfam; PP00144; Beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
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PLASMID=J3356/POX7/1;
MEDLINE=96422755; PubMed=8825372; DOI=10.1006/plas.1995.0005;
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Bacillales; Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                 Score 925; DB 2;
Pred. No. 2.2e-71;
); Mismatches 0;
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Pred. No. 2.2e-71;
; Mismatches 0;
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                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Mutant extended-spectrum beta-lactamase precursor (
Name=bla; Symonyms=blaTEM-116;
Bscherichia coli.
Plasmid pRP4, and Plasmid pCAPs.
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Q79DR3;
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Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serebrijski I., Vassin V., T
Submitted (JUL-1995) to the
EMBL; U31280; AAC44581.1; -.
HSSP; P00807; 1ALQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methylobacillus flagellatum.
Methylobacillus flagellatum.
Methylobacieria; Betaproteobacteria; Methylophilales;
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
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           SEQUENCE
                            NCBI_TaxID=562;
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InterPro; IPR000871; Beta_lactamase_A.
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'S; PR00118; BLACTAMASEA.
TE; PS00146; BETA_LACTAMASE_A; 1
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           FROM N.A.
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Pred. No. 2.2e-71;
; Mismatches 0;
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RESULT
Q38212
ID Q3
AC Q3
DT 01
DT 01
DT 0
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RT "Molecular Characterization of Extended-Spectric Produced by Clinical Isolates of Klebsiella pne coli from a Korean Nationwide Survey,";

RL J. Clin. Microbiol. 42:2902-2906(2004).

DR EMBL; M74750; AAA24457.1; -.

DR EMBL; M12694; CAA73226.1; -.

REMBL; AJ001614; CAA04868.1; -.

REMBL; AV425988; AAQ95605.1; -.

R EMBL; AV425989; AAQ95605.1; -.

R HSSP; P00807; 1AIQ.

GO; GO:0008800. P.*
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Bacteriophage f
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                                                                                                                                                                                                                                                                                                                                                                                                          Hydrolase; Plasmid;
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Schlieper D., Von
Mueller-Hill B.;
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Little M., Breitling F.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
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nia coli."
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                                                                                                                                                                                                                                                                                                                                                                                  286 AA;
 (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
ge f1-R208 ampicillinase gene mutation.
                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Von Wilcken-Bergmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=9514792; DOI=10.1006/abio.1997.2558; Wilcken-Bergmann B., Schmidt M., Sobek H.,
                                                                                                                                                                                                                                                                                                                                                                                                                      BETA LACTAMASE A;
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Pred. No. 2.2e-71;
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mutant
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Viruses; ssDNA vir
NCBI_TaxID=10863;
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SEQUENCE
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequen
05-JUL-2004 (TrEMBLrel. 27, Last annota
Inhibitor-resistant TEM beta-lactamase
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Topal M.D., Badie J.S., Conrad M.;
"O-6-methylguanine mutation and repair is nonuniform: Selection DNA most interactive with O-6-methylguanine.";
J. Biol. Chem. 261:9879-985(1986).
EMBL; M14017; AAA32208.1; -.
HSSP; Q9R435; HTZ.
                                                                                                                                                                        InterPro; IPR001466; Beta lactamase.
InterPro; IPR000871; Beta lactamase A.
Pfam; PF00144; Beta lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
                                                                                                                                                                                                                                                               Ghandili S. Hosseini-Mazinani S.M.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ
EMBL; AYSB376; AAS86427.1; -.
HSSP; P00807; IALQ.
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
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InterPro; IPR001871; Beta_lactamase_A.
Pfam; PF001144; Beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
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Last annotation update)
a-lactamase (Fragment).
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                    Score 920; DB 2; Length 232; Pred. No. 4.6e-71;
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ID 4H50
ID 2H50
ID 7D7
  RESULT 13
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ID Q84H4
AC Q84H4
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DT 01-JU
DT 01-OC
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Q84H49 PRELIMINARY;
Q84H49;
01-JUN-2003 (TrEMBLrel. 2:
01-JUN-2003 (TrEMBLrel. 2:
01-OCT-2003 (TrEMBLrel. 2:
TEM-110 beta-lactamase (F
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Ol-JUN-2003 (TrEMBLrel. 24, Created Ol-JUN-2003 (TrEMBLrel. 24, Last se Ol-OCT-2003 (TrEMBLrel. 25, Last ar TEM-117 beta-lactamase (Fragment). Escherichia coli.
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BOX A.T.A., Paauw A., Leverstein-vanHall M.A.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ eMBL; AY130282; AAN05026.1; -.

HSSP; Q9R435; 1HTZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001466; Beta_lactamase.
InterPro; IPR000871; Beta_lactamase_A.
Pfam; PF00144; Beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE_A; 1.
NON TEP
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Pred. No. 5.2e-71;
1; Mismatches 1
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Best Local S
Matches 179
Query Match
Best Local Similarity
Matches 179; Conserv
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NON_TER
SEQUENCE
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Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AYSB3762; AASB6428.1; -.
HSSP; P00807; 1ALQ.
InterPro; IPR001466; Beta_lactamase.
InterPro; IPR000871; Beta_lactamase_A.
Pfam; PF00144; Beta-lactamase_A.
Pfam; PF00144; Beta-lactamase_A.
PFNINTS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE_A; 1.
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InterPro; IPR000971; Beta_lactamase A.
Pfam; PF00144; Beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE_A; 1.
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Submitted (JUL-2002) to the
EMBL; AY130283; AAN05027.1;
HSSP; Q9R435; 1HTZ.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Acinetobacter sp. Ull.
Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q6PRU6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=269266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moraxellaceae; Acinetobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TEM beta-lactamase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q6PRU6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Klebsiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klebsiella oxytoca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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                                                                                                                                                     264
264 AA;
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261 AA;
       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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28738 MW;
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                                                                                                                                                 28986 MW;
                                 99.5%;
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to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 920; DB
Pred. No. 5.3e-
l; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
   Score 920; DB
Pred. No. 5.4e
1; Mismatches
                                                                                                                                                 A4F071CF7489352C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4F748F7733A08CBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             264
                                 DB 2;
5.4e-71;
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3e-71;
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databases.
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                                                                      Length 264;
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Search completed: June 10, Job time: 61.6383 secs

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Best Local
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05-JUL-2004
05-JUL-2004
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Yatsuyanagi J., Saito S., Harata S., Suzuki N., Amano K.
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY538700; AAS46846.1; -.
EMBL; AY538701; AAS46847.1; -.
EMBL; AY538702; AAS46848.1; -.
EMBL; AY538702; AAS46848.1; -.
EMBL; AY538698; AAS46848.1; -.
EMBL; AY538698; AAS46844.1; -.
EMBL; AY538698; AAS46844.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001466; Beta_lactamase.
InterPro; IPR000871; Beta_lactamase_A.
Pfam; PF00144; Beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE_A; 1.
NON TER
281
281
281
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Name=blaTEM-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLEL 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Serratia marcescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q6QIV0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TaxID=615;
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                                                                                                           144
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                                                                                                        KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPAAMATTLRKLLTGELLTLASRQ 203
                                                                                                                                             KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 180
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                                                                                                                                                                                                                          AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 143
                                                                                                                                                                                                                                                      AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLITTIGGP 120
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281 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30837 MW;
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98.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 920; DB 2;
Pred. No. 5.8e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C8934B9C696057BF CRC64;
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

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Minimum DB
Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM protein - protein search, using sw model
                                                                                                                              Database
                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                Title:
                                                                                                                                                                                                                      seq length:
seq length:
                                                                             US-10-668-778-2_COPY_1_190
975
                                                                                                                                                                                                                                                                                                                                                                                                                                        June 10, 2005, 10:22:36; Search time 73.6679 Seconds (without alignments) 997.510 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
                                                                                                                                                                                                                                                                                                 2105692 seqs, 386760381 residues
                                                                                                                                                                                                                                                                                                                               Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                 HPETLVKVKDAEDQLGARVG.......GELLTLASRQQLIDWMEADK 190
geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp2002s:*
geneseqp2003as:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2 2 2 5 4 3	221	19 20	18	16	15	13	12	Ħ	10	φ	œ	7	o	v	44	ω	N	1	ult No.
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ADR70416 ADR70428 AAU23219	ADR70410 ADR70404	ABR43622 ADR70422	ABP55474	AAB31173	AAB50898	AAB10438	AAB10442	AAY08529	AAW18679	AAW16635	AAR96423	AAR97619	AAR31575	AAW18680	AAW16634	ADJ67709	AAB36692	AAE05544	ID
Adr70416 Vector pA Adr70428 Vector pA Aau23219 Novel hum	Vector Vector	Abr43622 Cloning v Adr70422 Vector pA	Abp55474 Vector pC		Aab50898 Protein e	Aab10438 Expressio			Aaw18679 Secretory			_		Aaw18680 Intracell	Aaw16634 Beta-lact	Adj67709 Escherich	Aab36692 Escherich	Aae05544 E. coli	iption

13-JAN-2000; 2000US-0175968P. 15-MAR-2000; 2000US-00526106.

16-JAN-2001; 19-JUL-2001.

2001WO-US001651.

	44	43	42	41	40	39	38	37	36	35 5	34	<u>ω</u>	32	31	30	29	28	27	26
970	970	970	974	974	974	974	. 974	975	975	975	975	975	975	975	975	975	975	975	975
99.5	99.5	99.5	99.9	99.9	99.9	99.9	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
265	265	265	1967	1293	1293	872	286	2761	2307	2307	2307	1277	1088	1031	585	408	327	327	290
N	N	N	σ	7	7	7	N	N	w	w	w	N	N	ຫ	σ	σ	N	N	4
AAW48613	AAY08232	AAY08234	ABB82793	ADH14284	ADC22811	ADK65686	AAY06551	ADH11249	AAY70066	AAY70065	AAY70064	AAR52701	AAR88636	ADI46109	ADA67747	ABR55981	AAW18681	AAW16636	AAM84362
Aaw48613	Aay08232	Aay08234	Abb82793	Adh14284	Adc22811	Adk65686	Aay06551	Adh11249	Aay70066	Aay70065	Aay70064	Aar52701	Aar88636	Adi46109	Ada67747	Abr55981	Aaw18681	Aaw16636	Aam84362
Escherich	E. coli R	E. coli R		Vector pC	Human G p	-	Escherich		Recombina	Recombina		Plasmid p		Single st	Beta-lact	hCG beta-	. Membrane-	Beta-lact	Human imm

ALIGNMENTS

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RESULT 1
AABO5544
ID AABO
XX AABO
XX AABO
XX AABO
XX Inte
XW Circ
XW W020
XW Circ
XW W021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE05544 standard; protein;
                                                                                                                                                              Cleavage-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE05544;
                                                                                                              WO200151629-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coli mature TEM-1 beta-lactamase.
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                                                                                                                                                              /note= "BI
228. .229
                                                                                                                                                                                                                                                                                                                              149. .150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers 27. .28
                                                                                                                                                                                                202. .203
                                                                                                                                             note= "Break-point between alpha and omega fragments"
                                                                                                                                                                                                              note= "Break-point between alpha
                                                                                                                                                                                                                                              note= "Inter-sub-domain loop"
                                                                                                                                                                                                                                                               .89. .204
                                                                                                                                                                                                                                                                             note= "Break-point between alpha and
                                                                                                                                                                                                                                                                                              172. .173
                                                                                                                                                                                                                                                                                                             note= "Break-point between alpha
                                                                                                                                                                                                                                                                                                                                                                                               note=
                                                                                                                                                                                                                                                                                                                                                                                                                              note= "Inter-sub-domain loop"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "Break-point between alpha and omega fragments"
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                                                                                                                                                                               "Break-point between alpha and omega
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CC (IERA) systems that comprises a fusion sequence that encodes for a circularly permutated, interaction-activated proteins which produce a comprise a fusion sequence that encodes for a comprise of the control of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interaction-dependent enzyme association systems for detecting interactions between two or three polypeptides, especially in human therapeutics, diagnostics or prognostics, comprise circularly permutated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       domains, alpha-omega
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DB; AAD10411.
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                                                                                                                                                                                 KELTAFLHNMGDHVTRLDRWEPELNEAIENDERDTTMPVAMATTLRKLLTGELLTLASRQ
                                                                                                                                                                                                                                                                                                                                AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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QLIDWMEADK 190
                                                                      QLIDWMEADK 190
                                                                                                                                                                                                                                                                                    AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; ilarity 100.0%; Conservative
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Pred. No. 6.6e-98;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 263;
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121

KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ

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                                                                                                                                                                                                                                                                                                                           The present invention describes a fragment complementation system (I) CC which comprises a first oligopeptide (OP1) containing an N-terminal CC fragment with a C-terminal break point and a second oligopeptide (OP2) CC comprising a C-terminal with a N-terminal breakpoint, in which the C and CC N terminal fragments are both derived from a marker protein (MP) and CC reassemble to form a functionally reconstituted MP. Methods from the CC present invention are used for monitoring the occurrence of protein. CC protein interactions in a sample, identifying oligopeptide interactions CC protein interactions in a sample, identifying oligopeptide interactions CC protein interactions in a sample, identifying interactions between a maximum superior of a transmentance protein and a polypeptide, for compounds that bind to an extracellular domain of a transmentance protein and a polypeptide, for regulated signal transducers, forming a enzyme complementation system for selecting simultaneous incorporation of multiple genetic elements into a fost cell and for activating a beta-lactam derivative of an antitumour compound in a host who is in need of it. The present sequence represents the tell first in factor of the Becherichia coli mature TEM-1 beta-lactamase, which is used in the
                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel fragment complementation system to identify interactions between polypeptides comprises fragment pairs having first and second members that reassemble into a marker protein which has a directly detectable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
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                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 2; 94pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Balint RF, Her J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAY-1999; 99US-0135926P.
13-JAN-2000; 2000US-0175968P.
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                                                                                                                                                                                                                                                                                                               exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PANO-) PANORAMA RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-032034/04.
               121
                                                                                                                                                                                                     190;
                                                     61
                                                                                        61
                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                             263
KELTAFLHNMGDHYTRLDRWEPELNEAIPNDERDTTMPVAMATTIRKLLTGELLTLASRQ
                                                     AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                         AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                                            HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                                                                                                                                                HPETLYKVKDAEDQLGARVGYIELDLNSGKILESERPEERFPMMSTFKVLLCGAVLSRID
                                                                                                                                                                                                  100.0%; Score 975; DB 4;
larity 100.0%; Pred. No. 6.6e-98;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                           A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          beta-lactamase protein sequence
                                                                                                                                                                                                                                      Length 263;
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RESULT 3
ADJ67709
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                CC a first oligopeptide having an N-terminal fragment with a C-terminal CC break-point, and a second oligopeptide having a C-terminal fragment with a C-terminal CC a N-terminal fragment with a C-terminal CC a N-terminal fragment with a C-terminal fragment and the C-CC terminal fragment each are derived from a marker protein and reasemble component of the component of the component of the component of the first and second oligopeptide to which a first oligopeptide binds, involving co-cxpressing the first and second oligopeptide results in the functional CC expressing the marker protein. The method is also useful for identifying a CC expressing the courrence of protein. The method is also useful for considering the occurrence of protein. The method is also useful for consitoring the occurrence of protein. The method is also useful for consitoring the occurrence of protein protein interactions in a sample; CC and identifying epitopes that bind to an immunoglobulin variable region. CC (I) or an expression casette (II), encoding a selectable N or C-terminal component of a transmembrane protein and a polypeptide, where the cc inhibit, chosmonorylation is an immune cell protein, preferably CD40. (I) or consistent of high-throughput identification of compound that consistent consistency of the consistency of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fragment complementation system for detecting immunoglobulin epitope, has first oligopeptide containing N-terminal fragment with C-terminal break-point, second oligopeptide containing C-terminal fragment with N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    functional reassembly; protein-protein interaction; proteome interaction;
immunoglobulin variable region; immune cell protein; CD40;
phosphorylation-regulated cell signal transducer; TEM-1 beta-lactamase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADJ67709 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-SEP-2003; 2003US-00668778.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli TEM-1 beta-lactamase.
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DB; ADJ67708.
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RESULT 4
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Best Local S
Matches 190
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                                                                     Molecular chimaera for gene or virus directed enzyme prodrug therapy useful for treatment of cancer, viral infection or inflammation.
                                                                                                                                                                                                                                                                                                                                                                       Beta-lactamase (including signal
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                                                                                                                                     Dev I,
                                                                                                                                                                             20-NOV-1995;
                                                                                                                                                                                                                                                                                                          Escherichia coli
                                                                                                                                                                                                                                                                                                                                                   Gene directed enzyme prodrug therapy; GDEPT;
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                                                                                                                                                                                                                                                                                                                                       prodrug therapy; VDEPT; beta-lactamase; cancer;
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Escherichia coli beta-lactamase (AAW16634), including the signal peptide, is the expression product of a molecular chimaera, designated pCMV-BL (AAT66737), in which the beta-lactamase gene is under control of the CMV intermediate/early promoter. Vectors consisting of a transcriptional

English

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RESULT 5
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Best Local
                                                     The intracellular form (AAW18680) of TEM beta-lactamase is expressed by pCMV-delBL (AAT70311) in which a PCM-amplified beta-lactamase coding sequence, minus the signal sequence, is placed under control of the intermediate/early promoter of cytomegalovirus. Intracellular beta-lactamase constructs, placed under control of promoter/enhancer elements
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Secretion of the enzyme has the advantage of increasing neighbouring cell
                                                                                                                                                                                                                                                                          DNA construct for gene-directed enzyme prodrug therapy of lung cancer comprises lung- or neuroendocrine-specific promoter controlling expression of prodrug-converting enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prodrug therapy; gene directed enzyme prodrug therapy; GDEPT; virus directed enzyme prodrug therapy; VDEPT; lung cancer;
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                               lung-associated protein or neuroendocrine
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DB; AAT70311.
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Pred. No. 6.6e-98;
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                                                                                                                                                                                                                                                 Col 21-24; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hines RN,
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Pred. No. 6.6e-98;
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The expression constructs pRNH127 and pRNH155 contain identical sequences but were constructed using different strategies (see AAQ36498). The constructs comprise exons 2-7 of human CYP1A1 gene under the construct of the inducible mouse metallothionein (MMT-1) promoter. The constructs also contain an open reading frame in the opposite orientation to the cytochrome P450 exons. This ORF encodes ampicillin resistance. The constructs are suitable for transformation of human fibroblasts derived from the xeroderma pigmentosum group A. Cultures of the transformed from the xeroderma pigmentosum group A. Cultures of the transformed from the xeroderma pigmentosum group A. Cultures of the transformed from the xeroderma pigmentosum group A. Cultures of the transformed from the xeroderma pigmentosum group A. Cultures of the transformed from the xeroderma pigmentosum group A. Cultures of the transformed from the xeroderma pigmentosum group A. Cultures of the transformed from the xeroderma pigmentosum group A. Cultures of the transformed from the xeroderma pigmentosum group A. Cultures of the xeroderma pi

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                       A secretory beta-lactamase (AAR97619) is expressed from DNA construct pCMV-BL (AAT29220), in which the beta-lactamase coding sequence is under the control of the intermediate/early cytomegalovirus promoter. Beta-lactamase delivery to mammalian cells confers sensitivity to cephalosporin prodrugs. Liposomal DNA/5-fluorouracil prodrug combinations resulted in s.c. tumour regression in mice bearing As49 tumours. Survival of mice bearing human large cell lung H460 intrathoracic (i.t.) tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene therapy; gene directed enzyme prodrug therapy; GDEPT; virus directed enzyme prodrug therapy; VDEPT; prodrug activation; cytotoxic; cytostatic; cancer; tumour; retrovirus; vector;
                                                                                                                                                                                                                                                                                                              Molecular chimaera for use in enzyme gene therapy - is activated target cell to express a secretable enzyme which cleaves a prodruoutside the cell into a cytotoxic or cytostatic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR97619
                                                                                                                                                                                                                                                           Example 3; Page 57-58; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-268615/27.
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Pred. No. 7.4e-98;
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Matches 190;
The present sequence is encoded by a chimeric mouse metallothionein-cytochrome P450IAI (CYPIAI) expression construct. Two clones, pRNH127 and pRNH15, were isolated by different methods and which both had the same sequence. The CYPIAI construct is used in assays to test for cytotoxicity of humans to a chemical. The method comprises exposing human fibroblast cells normally not including any cytochrome P450 activity to potentially toxic chemicals. The cells having been transformed to express cytochrome P450, under the control of a controllable promoter through the CYPIAI gene, upon exposure to the chemical in vitro. The chemical is metabolised intracellularly into a cytochrome metabolite by oxidation within the
                                                                                                                                                                                                                                                                                                                                            Testing chemicals for cytotoxicity to human by using recombinant fibroblasts transformed with control of inducible promoter.
                                                                                                                                                                                                                                                                                           Disclosure; Col 17-24; 26pp; English.
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09-DEC-1992;
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25-NOV-1996
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Pred. No. 7.4e-98;
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                        Escherichia coli beta-lactamase (AAW16635), lacking the signal peptide, is the expression product of a molecular chimaera, designated pCMV-delBH (AAT66738), in which the beta-lactamase gene is under control of the CM intermediate/early promoter. Vectors consisting of a transcriptional regulatory DNA sequence linked to a beta-lactamase gene can be used for enzyme prodrug therapy. Intracellular expression of the beta-lactamase i a targetted cell allows conversion of a prodrug into an agent toxic to the cell for treatment of cancer, viral (e.g. HIV) infection or
                                                                                                                                                                                                                                                                                                                             Molecular chimaera for useful for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-1997
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                                                                                                                                                                                                                                                                           Example;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beta-lactamase (no signal peptide).
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s directed enzyme prodrug therapy; VDEPT; beta-lactamase;
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cancer, viral infection or inflammation.
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Pred. No. 7.4e-98;
; Mismatches 0;
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d pCMV-delBL
l of the CMV
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Best Local
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                                                                               comprises lung- or neuroendocrine expression of prodrug-converting
                                                                                         DNA construct for gene-directed enzyme prodrug therapy of lung cancer comprises lung- or neuroendocrine-specific promoter controlling
                                                                                                                                                                                                                                                                                                                                                                                        13-AUG-1997
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                                                                                                                                                                                                                                                                                                                                  beta-lactamase; pCMV-BL.
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                                                                                                                                                                                                                                                                                                                                                                     Secretory beta-lactamase
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                                                                                                                                                                                                                                                                                                                                                                                                                          standard; protein; 286
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                                                                                                                                                                  GROUP
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/label= Mat_protein
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                                                                                                                                               Sethna
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Pred. No. 7.4e-98;
; Mismatches 0;
                                                              English.
                                                                                enzyme.
                                                                                                                                                                                                                                                                                                                                            therapy; GDEPT;
lung cancer;
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The secreted form (AAW18679) of TEM beta-lactamase is expressed by BL (AAT70309) in which a PCR-amplified beta-lactamase coding sequen placed under control of the intermediate/early promoter of cytomegalovirus. Secretory beta-lactamase constructs, placed under control of promoter/enhancer elements of lung- associated protein of control of promoter/enhancer elements of lung- associated protein of the control of promoter elements of lung- associated protein of the control of promoter elements of lung- associated protein of the control of promoter elements of lung- associated protein of the control of promoter elements of lung- associated protein of the control of promoter elements of lung- associated protein of the control of promoter elements of lung- associated protein of the control of promoter elements of lung- associated protein of the control of promoter elements of lung- associated protein of the control of promoter elements of lung- associated protein of the control of promoter elements of lung- associated protein of the control of promoter elements of lung- associated protein of the control of promoter elements of lung- associated protein of the control of promoter elements of lung- associated protein of the control of promoter elements of lung- associated protein of the control of promoter elements of lung- associated protein of the control of promoter elements of lung- associated protein of the control of the cont

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This invention describes a novel tetracycline assay that uses recombinant prokaryotic cells comprising a luciferase gene under the transcriptional control of a tetracycline repressor and tetracycline promoter and involves the detection of luminescence emitted form the cells. The assay can be used to distinguish tetracycline form other microbial agents. The invention also describes a novel plasmid comprising either the luxCDABE genes, a tetracycline repressor (TetR) and a tetracycline promoter (TetA) from Tn10, or the insect luciferase gene, a tetracycline assay and a tetracycline promoter (TetA) from Tn10. The tetracycline assay method can be used for the determination of tetracycline in a sample,
                                                                                                                                                                        Assaying
                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Firefly; luciferase; tetracycline; transcriptional control; TetA; TetA; tetracycline repressor; tetracycline promoter; luminescence; luxCDABE; insect; Tn10; medicine; dosage; cheese production; antibiotic; foodstuf
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DB; AAV72418.
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                                                                                                                                                                       for tetracycline using recombinant prokaryotic cells
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                                                                                                                                                                                                                                        Karp M,
                                                                                                                                              Page 47-48; 67pp; English.
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Pred. No. 7.4e-98;
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Best Local
This invention describes a novel method for the selection of monoclonal antibodies (MAb) which comprises (i) fusing B lymphocytes with myeloma cells to produce antibody-producing hybridomas such that the antibodies are presented at the surface of the hybridomas by an antibody-binding protein (I); and (ii) binding the antibody to antigens (Ag). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e.g. to study the dosage and penetration of the medicine. The method can also be used to test cheese production, as cheese making bacteria are not able to work in the presence of tetracycline. The method can also be used to determine the presence or concentration of antibiotics in foodstuffs, e.g. for allergic people. The present assay method does not rely on the growth of microbes as do conventional tests, and so is much more rapid. The present assay is also more sensitive, as even a small amount of luminescence can be detected
                                                                                                                                 Selecting monoclonal antibodies, by expressing them on the surface hybridomas attached to antibody-binding protein, then reaction with
                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                           Expression vector; antibody binding protein; monoclonal antibody; Neo-R; B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.
                                                                                         Claim 16;
                                                                                                                                                                                                                        Breitling F,
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                                                                                                                                                                                                                                                                                                             11-JAN-1999;
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                                                                                      Fig 3; 22pp; German.
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Pred. No. 7.4e-98;
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RESULT 13
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OX Synth
XX DE195
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XX II-JJ
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                                                                                                                                                   Selecting monoclonal antibodies, by expressing them on the surface of hybridomas attached to antibody-binding protein, then reaction with antibody library.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Breitling F,
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100.0%; P
vative 0;
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Pred. No. 7.4e-98;
); Mismatches 0;
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Claim 16; Fig 1; 22pp; German

Selecting monoclonal antibodies,

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RESULT 14
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AC AABIO
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XX Expre
XX Expre
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KW Expre
KW Expre
XX DE199
XX JE199
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XX 11-JA
XX 11-JA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                    N-PSDB; AAA71429
                                                                                                                                                                                                                                                                                                                                                     Expression vector; antibody binding protein; monoclonal antibody; Neo-R; B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.
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                                                         WPI; 2000-499832/45.
                                                                                        Breitling
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                                                                                                                                                                                                       11-JAN-1999;
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                                                                                              Moldenhauer G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC This invention describes a novel method for the selection of monoclonal CC antibodies (MAb) which comprises (i) fusing B lymphocytes with myeloma CC cells to produce antibody-producing hybridomas such that the antibodies CC are presented at the surface of the hybridomas by an antibody-binding CC protein (I); and (ii) binding the antibody to antigens (Ag). The CC invention also describes antibody-binding proteins (I) that comprise a CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa CC chain or a murine MHC (major histocompatibility complex) Class I k(k) CC molecule; an antibody-binding site of proteins A, G, L or LG, and the CC transmembrane domain of PDGPR (platelet-derived growth factor receptor) CC or CD52. The method is used to select MAb with specificity for particular CC antigens. MAb can be selected without separate culture of hybridomas, and CC cost involved in Mab selection. This sequence represents the time and CC cost involved in Mab selection. This sequence represents the bla protein CC bla protein, Neo-R and protein G described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 975; DB 3; Best Local Similarity 100.0%; Pred. No. 7.4e-98; Matches 190; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                      bla resistance marker; recombinant host cell; saccharification; fermentation; polysaccharase; oligosaccharide degradation; celz glucanase; integration vector; pLO12306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hybridomas attached to antibody-binding protein, then reaction with antibody library.
                                                  26-MAY-1999;
                                                                                 26-MAY-2000; 2000WO-US014773
                                                                                                                      30-NOV-2000
                                                                                                                                                      WO200071729-A2
                                                                                                                                                                                                                                                                                             Protein encoded by bla resistance marker of integration vector pLO12306.
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                (UYFL ) UNIV FLORIDA RES FOUND
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Search completed: June 10, 2005, 10:49:12 Job time: 73.6679 secs

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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              into cells to generate recombinant host cells. The vector contains a surrogate promoter from Zymomonas mobilis, the celZ gene from Erwini chrysanthemi, resistance markers bla and tet, and Klebsiella oxytoca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           control of a surrogate promoter capable of increasing expression of the polysaccharase. The host cell also contains a second heterologous polymucleotide encoding a secretory polypeptide to facilitate the secretion of the expressed polysaccharase. The recombinant host cell is useful for producing polysaccharase which is useful for enzymatically degrading oligosaccharides such as lignocellulose, hemicellulose, cellulose, pectin or their combinations, and fermenting the product to ethanol, by simultaneous saccharification and fermentation processes. The present sequence is encoded by an integration vector which was introduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is given in a specification relating to a recombinant host cell suitable for simultaneous saccharification ar fermentation. The host cell contains at least one heterologous polynucleotide encoding a polysaccharase under the transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 286 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 82-83; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant host cells useful for producing polysaccharase for degrading oligosaccharides, comprises a first heterologous polynucleotide encoding polysaccharase under control of surrogate promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             target sequence
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                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                       QLIDWMEADK 190
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QLIDWMEADK 213
                                                                                KELTAFLHIMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRO
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/ECTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-23-933-14
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US-09-23-933-21
US-09-23-769B-362
US-09-025-769B-362
US-09-919-901-7
US-09-919-901-21
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US-09-490-153-362
US-09-490-153-362
US-09-490-153-362
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728.091 Million cell updates/sec
Sequence 2, Appli
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Sequence 14, Appl
Sequence 26, App
Sequence 26, App
Sequence 14, Appl
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Sequence 14, Appl
Sequence 27, Appli
Sequence 21, Appl
Sequence 26, App
Sequence 36, App
Sequence 36, App
Sequence 14, Appli
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Sequence 27, Appli
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Sequence 285, App
Sequence 362, App
Sequence 285, App
Sequence 285, App
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
970	974	974	974	974	975	975	975	975	975	975	975	975	975	975	975	975	975
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US-08-407-544-2	US-09-364-425B-57	US-09-170-496D-292	US-10-231-013-9	US-09-555-510B-9	US-10-191-966-16	US-10-191-966-9	US-10-191-966-2	US-09-919-901-16	US-09-919-901-9	US-09-919-901-2	US-09-263-933-16	US-09-263-933-9	US-09-263-933-2	US-09-490-324-300	US-09-490-324-298	US-09-490-324-285	US-09-490-153-300
Sequence 2, Appl	Sequence 57,	Sequence 292, Ap	Sequence 9, A	Sequence 9, Appl	Sequence 16, Appl	Sequence 9, Appl	Sequence 2, Appl	Sequence 16, App	Sequence 9, Appl	Sequence 2, Appl:	Sequence 16, App	Sequence 9, Appli	Sequence 2, A	Sequence 300, App	Sequence 298,	Sequence 285,	Sequence 300,

ALIGNMENTS

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RESULT 1
US-07-721-775A-2
; Sequence 2, Application US/07721775A
; Patent No. 5180666
; GENERAL INFORMATION:
; CENTRAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 286 aming
                                                                        Matches 190;
                                                                                          Query Match
Best Local Similarity
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/721,775A
FILING DATE: 19910627
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REGISTRATION NUMBER: 30,955
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APPLICANT: Hines, Ronald N.
APPLICANT: NO. 5180666sk, Raymond F.
TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL
                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
                                                                                                                                                                 TOPOLOGY: 15
MOLECULE TYPE:
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P.O. Box 4390
                                                                        Conservative
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                                                                        100.0%; Score 975; DB 1; 100.0%; Pred. No. 1e-107; tive 0; Mismatches 0;
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AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120

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181 QLIDWMEADK 190

KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 180

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                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-339-658-2
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/339,658

FILING DATE: 15-NOV-1994

CLASSIFICATION NUMBER: US 07/990,295

FILING DATE: 09-DEC-1992

APPLICATION NUMBER: US 07/990,295

FILING DATE: 09-DEC-1992

APPLICATION NUMBER: 09-DEC-1992

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 9-321WSU

TELEPHONE: (313) 689-3554

TELEPHONE: (313) 689-3554
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                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT: No. 5525482ak, Raymond F.

TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL
NUMBER OF SEQUENCES: 2
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ADDRESSEE: Releing, Ethington, Barnard, Perry & Milton STREET: P.O. Box 4390
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                                                                                                                                                                                                                                                                   y Match 100.0%;
Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 286 amino acids TYPE: amino acid TOPOLOGY: linear
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                     KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLIGELLTLASRQ 180
                                                                                                       AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
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KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRO 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (313) 689-4071
(317) TN NO: 2:
                                                                                                                                                                                                                                                      Conservative
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APPLICANT: Jockson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

ITILE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/09/263,933

CURRENT FILING DATE: 1999-03-08

EARLIER FILING DATE: 1998-08-05

NUMBER OF SEQ ID NO: 33

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO: 7

LENGTH: 286

TYPE: PRT

ORGANISM: Artificial Sequence

US-09-263-933-7
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US-09-263-933-14
; TYPE: PRT ; ORGANISM: Artificial Sequence US-09-263-933-14
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                                                                                    GENERAL INFORMATION:

APPLICANT: Potts, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT TAPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14, Application US/09263933 Patent No. 6280940
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Best Local Similarity
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                                                                     LENGTH: 286
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Sequence 21, Application US/09263933

Patent No. 6280940

GENERAL INFORMATION:

APPLICANT: Potte, Karen E.

APPLICANT: Potte, Karen E.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

FILE REPERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/09/263,933

CURRENT APPLICATION NUMBER: 09/129,611

EARLIER APPLICATION NUMBER: 09/129,611

EARLIER FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 21

LENGTH: 286

TYPE: PRT

ORGANISM: Artificial Sequence

US-09-263-933-21
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                                                  Sequence 265, Applicate Patent No. 6300064
GENERAL INFORMATION:
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Best Local
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Best Local Similarity 100.0%;
Matches 190; Conservative 0;
               APPLICANT:
APPLICANT:
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                                                                                     Application US/09025769B
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             Knappik, Achim
Pack, Peter
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Pred. No. 1e-107;
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APPLICANT: Ge, LANGE, Simon
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Near
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                 RESULT 7
US-09-025-769B-362
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                                                                                                                                                                                                                                  Sequence 362, Application US/09025769B
Patent No. 6300064
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Best Local S
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ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEPHAX: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO:
                                                              APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
APPLICANT: Plueckthun, Andreas
                                                                                                                                                                                                              GENERAL INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILLING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
TITLE OF INVENTION: Protein/(Poly)peptide libraries NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                            TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
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203

83 60 0

STREET: 1251 AVCCITY: New York
STATE: New York

USA

ADDRESSEE: James F. STREET: 1251 Avenue

Haley, Jr., Esq. c/o Fish & Neave of the Americas

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CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-09-025-769B-362
                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FBB-1998
FILING DATE: 18-FBB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-NGC-1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09919901 Patent No. 6599738
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y Match 100.0%; Score 975; DB 3;
Local Similarity 100.0%; Pred. No. 1e-107;
nes 190; Conservative 0; Mismatches 0
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TYPE: amino acid
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(212)596-9090
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                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 14
LENGTH: 286
TYPE: PRT
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                                                                                                                                                                                                                                                              Matches 190;
                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR PILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0
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   181
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QLIDWMEADK 190
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                                        KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ
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100.0%; Pred. No. 1e-107;
tive 0; Mismatches 0;
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204 QLIDWMEADK 213

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CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/23,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
I PRIOR FILING DATE: 1998-08-05
I NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 21
SEQ ID NO 21
LENGTH: 286
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US-09-490-070A-265
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US-09-919-901-21
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GENERAL INFORMATION:
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Best Local (
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Patent No. 6599738
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APPLICANT: Jackson, Roberta L.
APPLICANT: PATCK, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
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                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe
                                                                                                                                                                              Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
ZIP: 20006
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                       APPLICANT: Knappik, Achim
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                                     CITY: Washington
STATE: D.C.
COUNTRY: USA
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                                                                                                  STREET: 1666 K Street, N.W., Suite 300
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Ilag, Vic
Ge, Liming
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US-09-490-070A-362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6696248
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 362, Application US/09490070A
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2000
INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 100.0%;
Local Similarity 100.0%;
ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/490,070A FILING DATE: 24-Jan-2000 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe
                                                                                                                                                                                                                                                                                                          Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 265:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Knappik, Achim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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                                                                                                                                              CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QLIDWMEADK 213
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                                                                                                                                                                                                                   STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                 Pack, Peter
Ilag, Vic
Ge, Liming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Pred. No. 1e-107;
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,070A

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; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 362: US-09-490-070A-362
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Patent No. 6706484
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 362: SEQUENCE CHARACTERISTICS:
                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEB: James F. Haley, Jr., Esq.
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
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                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                  Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Knappik, Achim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 286 amino acids
TYPE: amino acid
APPLICATION NUMBER: US/09/025,769B
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RESULT 14
US-09-490-153-362
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GENERAL INFORMATION:
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Best Local Similarity
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                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Unn-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley,
STREET: 1251 Avenue of the
                                                                                                                                                                                                                                                                                                                                                                                                  Moroney, Šimon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 265:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 18-95 11 3021.0 FILING DATE: 18-AUG-1995 ATTORNEY/AGENT INFORMATION:
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TELEPHONE: (212)596-9000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KELTAFIHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QLIDWMEADK 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGQEQLGRRIHYSQNDLVEYSFVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QLIDWMEADK 213
                                     APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                        STATE: New York
                                                                                                                                                                                                                                                                                                                         CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
APPLICATION NUMBER: EP 95 11 3021.0 FILING DATE: 18-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Knappik, Achim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peter
                                                                                                                                                                                                                                                                                                                                              Jr., Esq. c/o Fish & Neave
Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>,</u>
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LENGTH: 286 amino acids
TYPB: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 362:
US-09-490-153-362
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US-10-191-966-7
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                                                                                                                                                                                                                                                                                                                              SOPTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENCTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                    Query Match 100.0%; Score 975; DB 4; Length 286; Best Local Similarity 100.0%; Pred. No. 1e-107; Matches 190; Conservative 0; Mismatches 0; Indels
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Best Local Similarity
Matches 190; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Potts, Karen E.

APPLICANT: Potts, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/10/191,966

CURRENT FILING DATE: 2002-07-10

PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR PILING DATE: 1998-08-05

RUMBER OF SEQ ID NOS: 33

CONTANDE DESCRIPTION OF THE HEPATITIS C VIRUS PROTEANCE. WINDER

ROSENTANDE DATE: 1998-08-05
                                                                                                                                                                                                                                                                             FEATURE:
OTHER INFORMATION: :
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INFORMATION FOR SEQ ID NO: 362:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 27,794
REFERENCE FOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
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  61 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
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                                                                                   HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPWMSTFKVLLCGAVLSRID 60
                                                   HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 83
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Search completed: June 10, 2005, 11:01:16 Job time: 20.4801 secs

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Result
No.
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Compugen Ltd.
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C;Superfamily: beta-lactamase
C;Keywords: hydrolase
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A; Residues: 1-286 <WAC>
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from

GB/EMBL/DDBJ

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Saccharon

PIDN: CAA05686.1

415.5 40.3 306 1 B45822 beta-lactamase 419.5 39.8 306 2 G69674 beta-lactamase 409.5 39.7 288 2 J01136 beta-lactamase 409.5 39.6 306 2 S47330 beta-lactamase 408.5 39.6 306 2 S47330 beta-lactamase 408 39.5 305 2 A60156 beta-lactamase 408 39.5 305 2 A60680 beta-lactamase 408 39.5 305 2 A57002 beta-lactamase 408 39.5 305 2 A60680 beta-lactamase 508.5 39.3 304 2 A49789 beta-lactamase 5098.5 39.3 304 2 A49789 beta-lactamase 5098.5 38.6 288 2 JS0755 beta-lactamase 5098.5 38.6 288 2 JF0074 beta-lactamase 5093.5 38.1 2 JN0520 beta-lactamase 5093.5 38.1 263 2 S23929 beta-lactamase 5093.5 38.1 263 2 S23929 beta-lactamase 5093.5 37.7 311 1 S02714 beta-lactamase 5093.5 37.6 305 1 C45822 beta-lactamase 5093.5 37.6 305 1 C45822
306 1 B45822 306 2 G69674 288 2 JO1136 306 2 S47330 305 2 A61156 305 2 A57002 305 2 A57002 304 2 A49789 304 2 A35001 288 2 JS0755 311 2 JN0520 291 2 JP0074 263 2 S23929 276 3 S23929 311 1 S05268 311 1 C45822
1 B45822 2 G69674 2 JQ1116 2 S47330 2 A51050 2 A57002 2 A50680 2 A49789 2 A35001 2 JS0755 2 JP0074 2 JP0074 2 S23929 2 S23929 1 C45827
B45822 G69674 JQ1136 S47330 A61156 A57002 A60680 A59789 A35001 JS0755 JN0520 JP0074 S23929 S02714 C45822
beta-lactamase beta-lactamase beta-lactamase penicillinase beta-lactamase

ALIGNMENTS

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beta-lactamase (EC 3.5.2.6) - phage phi-X174
C;Species: phage phi-X174
C;Species: phage phi-X174
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S47061
R;Henrich, B.; Schmidtberger, B.
submitted to the EMBL Data Library, July 1994
A;Description: A variant of phiX174 gene E-based positive selection vectors with enhanced A;Reference number: S47060
A;Accession: S47061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 100.0%; Score 1032; DB 2; Similarity 100.0%; Pred. No. 1.2e-82; O; Mismatches O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
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C;Species: by hour C;Species: by hour C;Species: by hour C;Date: 25-Dec-1994 #sequence_revalue.
C;Date: 25-Dec-1994 #sequence_revalue.
C;Accession: $41975
R;Kaestner, K.H.; Montoliu, L.; Kern, H.; Thulke, M.; Schutz, R;Kaestner, K.H.; Montoliu, L.; Kern, H.; Thulke, M.; Schutz, R;Kaestner, K.H.; Montoliu, L.; Kern, H.; Thulke, M.; Schutz, R;Accession: Accession: Accession
beta-lactamase (EC 3.5.2.6) precursor - Escherichia N;Alternate names: beta-lactamase TEM-6 (for blaT-6 C;Species: Escherichia coli C;Date: 30-Nov-1980 #sequence_revision 01-Sep-1981 #
                                                                                                                                                         PNECP
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-286 <HEN>
A;Cross-references: UNIPROT:Q38058; EMBL:Z35638; NID:g520996; PIDN:CAA84692.1; PID:g5209
C;Superfamily: beta-lactamase I
C;Keywords: hydrolase
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A; Residues: 1-286 < KAE>
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Best Local Similarity
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Pred. No. 1.2e-82;
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                            01-Sep-1981 #text_change 16-Aug-2004
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A;Cross-references: GB:M32794; NID:g152521; PIDN:AAA26408.1; PID:g152522
A;Experimental source: PK2
R;Goussard, S.; Sougakoff, W.; Mabilat, C.; Bauernfeind, A.; Courvalin, P.
J. Gen. Microbiol. 137, 2681-2687, 1991
A;Title: An IS1-like element is responsible for high-level synthesis of extended-spectrum A;Reference number: S24415; MUID:92166702; PMID:1665171
A;Accession: S24415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: Beta-lactamase I
C;Keywords: antibiotic resistance; hydrolase; membrane protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-286/Product: beta-lactamase #status experimental <MAT>
F;68/Active site: Ser #status predicted
F;68/Active site: Ser #status predicted
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Cold Spring Harb. Symp. Quant. Biol. 43, 77-90, 1979

Cold Spring Harb. Symp. Quant. Biol. 43, 77-90, 1979

A;Title: Complete nucleotide sequence of the Escherichia coli plasmid pBR322

A;Reference number: A90923; MUID:80002802; PMID:383387

A;Contents: annotation
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A;Residues: 1-101, 'K',103-161,'H',163-286 <GOU>
A;Residues: 1-101,'K',103-161,'H',163-286 <GOU>
A;Cross-references: EMBL:X57972; NID:g41816; PIDN:CAA41038.1; PID:g41817
A;Experimental source: ISI-11ke blaT-6 DNA
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A;Title: The kil-kor regulon of broad-host-range plasmid RK2: nucleotide A;Reference number: A35387; MUID:90264294; PMID:2160936
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R;Ambler, R.P.; Scott, G.K.
Proc. Natl. Acad. Sci. U.S.A. 75, 3732-3736, 1978
A;Title: Partial amino acid sequence of penicillinase of A;Reference number: A93820; MUID:79012483; PMID:358199
A;Accession: A93820
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A: Pesidues: 1-286 <SUT>
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A; Title: Nucleotide sequence of the ampicillin resistance
A; Reference number: A93821; MUID:79012484; PMID:358200
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A;Residues: 24-36, K, 38-286 <AMB>
A;Residues: 24-36, K, 38-286 <AMB>
A;Rsperimental source: plasmid R6K
R;Kornacki, J.A.; Burlage, R.S.; E;
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A;Residues: 182-286 <KOR>
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QLIDWMEADKVAGPLLRSALPA
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pBR322
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Pred. No. 3.2e-82;
225
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R;Mabilat, C.; Lourencao-Vital, J.; Goussard, S.; Courvalin, P. Mol. Gen. Genet. 235, 113-121, 1992
A;Title: A new example of physical linkage between Tn1 and Tn21: the antibiotic multiple A;Reference number: S30112; MUID:93062798; PMID:1331747
A;Accession: S30113
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A;Residues: 1-286 <RES>
A;Residues: 1-286 <RES>
A;Crose-references: EMBL:U21228; NID:g885956; PIDN:AAA70411.1; PID:g885958
C;Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Taylor, J.; Stearman, R.S.; Uratani, B.B.
Plasmid 29, 241-244, 1993
A;Title: Development of a native plasmid as a cloning vector in Clavibacter xyli
A;Reference number: I40904; MUID:93361581; PMID:7889234
A;Accession: I40905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: synthetic
A;Note: cloning vector pCG1408 engineered and expressed in Clavibacter xyli
C;Date: 15-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Oct-2000
C;Accession: I40905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                beta-lactamase (EC 3.5.2.6) TEM-3 - Klebsiella pneumoniae plasmid pCFF04
C;Species: Klebsiella pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:P00810;
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Best Local Similarity
                                                                                                                                                                                                                                                                                             ;Superfamily: beta-lactamase I
;Keywords: antibiotic resistand
                                                                                                                                                                                                                                                                                                                                      Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                          ;Gene: bla(TEM-3)
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  KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 180
                                                                 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
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                                                                                                                            HPETLVKVKDAEDKLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRVD 83
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                                         AGQEQLGRRIHYSQNDLVKYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 143
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                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                          Score 1019; DB 2;
Pred. No. 1.6e-81;
3; Mismatches 1
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Pred. No. 3.2e-82;
1; Mismatches 1;
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extended spectrum beta-lactamase CAZ-2 - Klebsiella pneumoniae C;Species: Klebsiella pneumoniae C;Species: Klebsiella pneumoniae C;Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 22-Jun-1999 C;Accession: S6310 R;Chanal, C.; Poupart, M.C.; Sirot, D.; Labia, R.; Sirot, J.; Cluzel, R. Antimicrob. Agents Chemother: 36, 1817-1820, 1992 A;Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes. A;Reference number: S60310; MUID:93037315; PMID:1416873 A;Accession: S60310
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S60310
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A;Residues: 1-286 <CHA>
A;Cross-references: EMBL:X6525
C;Superfamily: beta-lactamase
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A;Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes. A;Reference number: S60310; MUID:93037315; PMID:1416873
A;Accession: S60312
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A; Residues: 1-286 < CHA>
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197; Conservative
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Similarity 97.5%;
                                                                            HPETLVKYKDAEDKLGARVGYIBLDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRVD 83
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AGGEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
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                                                                                                          HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60
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                                                                                                                                                                                           98.2%;
                                                                                                                                                                  Score 1013; DB 2;
Pred. No. 5.4e-81;
3; Mismatches 2
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Pred. No. 4.4e-81;
3; Mismatches 2;
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N;Alternate names: beta lactamase homolog
C;Species: Salmonella typhimurium plasmid
C;Date: 30-Sep-1993 #sequence revi-
                 A;Title: Complete nucleotide sequence and A;Reference number: JQ1538; MUID:92383313; A;Accession: JQ1546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-32 <TOL>
A;Cross-references: GB:M55547; NID:g155010; PIDN:AAA98408.1;
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                                                                                R; Cannon, P.M.; Strike, P. Plasmid 27, 220-230, 1992
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Plasmid 24, 218-226, 1990
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A; Residues: 1-286 < CHA>
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A;Status: translation
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HPETLVKVKDAEDKLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRVD 83
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97.5%;
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Pred. No. 5.4e-81;
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                                         gene organization ; PMID:1325061
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A;Genome: plasmid
C;Superfamily: bet
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A; Residues: 1-30,'L',32-286 < LEE>
A; Residues: 1-30,'L',32-286 < LEE>
A; Cross-references: GB: X62115; NID: g48988; PIDN: CAA44025.1; PID: g48990
A; Experimental source: plasmid BWH77
C; Genetics:
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R;Lee, K.V.; Hopkins, J.D.; Syvanen, M.
J. Bacteriol. 172, 3229-3236, 1990
A;Title: Direct involvement of IS26 in an antibiotic resistance
A;Reference number: A35395; MUID:90264317; PMID:2160941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Klebsiella pneumoniae C;Date: 21-Nov-1993 #sequence revision 10-Nov-1995 #text_char C;Accession: S16146; A35395, S18767 C;Accession: S16146; A35395, S18767 R;Podbielski, A.; Schoenling, J.; Melzer, B.; Warnatz, K.; Legen, Microbiol. 137, 569-578, 1991 Gen. Microbiol. 137, 569-578, 1991 A;Tile: Molecular characterization of a new plasmid-encoded A;Reference number: S16146; MUID:91237320; PMID:2033379
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S16146
beta-lactamase (EC 3.5.2.6) 2A precursor -
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A; Residues: 1-286 < CAN>
A; Cross-references: UNI
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C;Superfamily: beta-lactamase I
C;Keywords: antibiotic resistano
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A; Residues: 1-286 < POD>
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Best Local Similarity 67.7
Conservative
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                                                               GQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGFK 121
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ELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQQ 181
                                                                                                                         POPLEQIKOSESOLSGRVGMIEMDLASGRTLTAWRADERFPMMSTFKVVLCGAVLARVDA
                                                                                                                                                    PETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRIDA
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                                           GDEQLERKIHYRQQDLVDYSPVSEKHLADGMTVGELCAÄAITMSDNSAANLLLATVGGPA 142
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98.0%;
                                                                                                                                                                                                                                69.5%; Score 717; DB 2; 67.7%; Pred. No. 3.9e-55;
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Pred. No. 5.4e-81;
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A;Genome: plabuler (C;Superfamily: Beta-lactamase I C;Keywords: antibiotic resistance; hydrolase F;1-21/Domain: signal sequence #status predicted <SIG>F;1-21/Domain: signal sequence #status predicted <SIG>F;1-2
                                                                                                                                                                                                                                                                                                                          R;Barthelemy, M.; Peduzzi, J.; Labia, R.
Blochem. J. 251, 73-79, 1988
Biochem. J. 251, 73-79, 1988
A;Title: Complete amino acid sequence of p453-plasmid-mediated PIT-2
A;Reference number: S00464; MUID:88268817; PMID:3260490
A;Accession: S00464
                                                                                                                                                                                                                                                                                                                                                                                                                                                beta-lactamase (EC 3.5.2.6) class A - Escherichia coli plasmid p453 N;Alternate names: beta-lactamase PIT-2; beta-lactamase SHV-1 C;Species: Escherichia coli C;Species: Bscherichia coli C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1993 C;Accession: S00464 R;Barthelemy, M.; Peduzzi, J.; Labia, R.
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A;Title: Nucleotide sequence of SHV-2 beta-lactamase gene. A;Reference number: A60679; MUID:90351141; PMID:2201259
A;Accession: A60679
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A; Residues: 1-265
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A; Residues: 1-286 <GAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: not compared with conceptual translation
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                                 Query Match
Best Local S
Matches 136
                                                                                                                                                 ;Genome: plasmid
;Superfamily: beta-lactamase I
;Keywords: antibiotic resistance; hydrolase
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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;Accession: A60679
                                                                                                                                                                                                                                             Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics:
                                 Watch 69.1%; Score 713; DB 2; Local Similarity 67.7%; Pred. No. 7.9e-55; Pes 136; Conservative 29; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIDWMEADKVAGPLLRSALPA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDEQLERKIHYRQQDLVDYSPVSEKHLADGWTVGELCAAAITMSDNSAANLLLATVGGPA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLOWNVDDRVAGPLIRSVLPA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PETLYKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRIDA 61
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Pred. No. 3.9e-55;
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                                                                                         Length 265;
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A;Molecule type: DNA,
A;Residues: 1-286 <HUL,
A;Residues: 1-286 <HUL,
A;Cross-references: UNIPROT:P14558; GB:M95179; NID:g150488; PIDN:AAA25526.1; PID:g150489
A;Cross-references: UNIPROT:P14558; GB:M95179; NID:g150488; PIDN:AAA25526.1; PID:g150489
R;Podbielski, A.; Melzer, B.
Nucleic Acids Res. 18, 4916, 1990
Nucleic Acids Res. 18, 4916, 1990
A;Title: Nucleotide sequence of the gene encoding the SHV-2 beta-lactamase (bla(SHV-2)) of A;Reference number: S12703; MUID:90370479; PMID:2395654
                                                                                                                                                                                                                                    R;Huletsky, A.; Couture, F.; Levesque, R.C. Antimicrob. Agents Chemother. 34, 1735-1732, 1990
A;Title: Nucleotide sequence and phylogeny of SHV-2 beta-lactamase A;Reference number: A44998, MUID:91136192; PMID:2285285
A;Accession: A44998
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S02434
                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Klebsiella ozaenae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
C;Accession: A44998; S12703
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A;Title: Single amino acid substitution between SHV-1 beta-lactamase A;Reference number: S02434; MUID:88196385; PMID:3129309
A;Accession: S02434
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A;Residues: 1-265 <BAR>
C;Superfamily: beta-lactamase I
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                                                                                                                                                                                                           A;Status: preliminary
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; Pred. No. 7.9e-55;
29; Mismatches 36
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A;Accession: S12703
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-286 <PODD
A;Crose-references: EMBL:X53433; NID:g43789; PIDN:CAA37524.1; PID:g43790
C;Genetics:
A;Genome: plasmid
C;Superfamily: Beta-lactamase I
C;Superfamily: Beta-la
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Result
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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-lactamase (EC	beta	A49789	N	304	37.7	367.5	ω
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-lactamase (EC	beta	JQ1136	N	288	38.1	371.5	μ,
-lactamase (EC	beta	JL0091	N	310	38.2	372	0
-lactamase (EC	beta	C45822	۳	305	38.3	373.5	9
-lactamase (EC	beta	S23929	N	263	38.8	378.5	œ
-lactamase (EC	beta	JP0074	N	291	39.0	380.5	7
beta-lactamase (EC	beta	A60680	N	305	39.1	381	σ
-lactamase (EC	beta	A57002	ผ	305	39.1	381	u
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enicillinase - Ba	penı	847330	N	306	39.9	389.5	w
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-lactamase (EC	beta	G69674	N	306	•	395.5	Р
beta-lactamase (EC	рега	S42075	N	291	40.9	398.5	0

ALIGNMENTS

RESULT 1

T51301

T51301

beta-lactamase (BC 3.5.2.6) - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Species: Schizosaccharomyces pombe

C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000

C;Accession: T51301

C;Accession: T51301

C;Accession: T51301

C;Accession: T51301

C;Accession: T51301 RESULT 2
\$47061
beta-lactamase (EC 3.5.2.6) - phage phi-X174
C;Species: phage phi-X174
C;Species: phage phi-X174
C;Species: phage phi-X174
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: \$47061
R;Henrich, B.; Schmidtberger, B.
submitted to the EMBL Data Library, July 1994
A;Bescription: A variant of phiX174 gene E-based positive selection vectors with enhanced A;Reference number: \$47060
A;Accession: \$47061 A;Gene: bla C;Superfamily: beta-lactamase C;Keywords: hydrolase A;Cross-references: EMBL:AJ002683; C;Genetics: Yeast 13, 1065-1075, 1997
A;Title: Heterologous HIS3 marker and GFP reporter modules for PCR-targeting in Saccharon A;Reference number: Z09587
A;Accession: T51301 A; Molecule type: DNA A; Residues: 1-286 < WAC> A;Status: preliminary; translated h 100.0%; Score 975; DB 2; Similarity 100.0%; Pred. No. 5.8e-80; 90; Conservative 0; Mismatches 0; QLIDWMEADK 190 KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 180 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID HPETLYKYKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID OLIDWMEADK 213 KELTAFLHNMGDHVTRLDRWEPELNEAI PNDERDTTMPVAMATTLRKLLTGELLTLASRO from GB/EMBL/DDBJ PIDN:CAA05686.1 Length 286; Indels · 0; Gaps 83 143 0

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A;Molecule type: DNA
A;Residues: 1-286 <KRE>
A;Cross-references: EMBL:X76682; NID:g453622; PIDN:CAA54104.1; PID:g453623
A;Note: submitted to the EMBL Data Library, December 1993
C;Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: synthetic
C;Date: 25-Dec-1994 #sequence_revision 22-Aug-1996 #text_change 20-Oct-2000
C;Accession: S41975
R;Kaesther, K.H.; Montoliu, L.; Kern, H.; Thulke, M.; Schutz, G.
Gene 118, 67-70, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q38058; EMBL:Z35638; NID:g520996; PIDN:CAA84692.1; PID:g5209
C;Superfamily: beta-lactamase I
C;Keywords: hydrolase
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A;Molecule type: DNA
A;Residues: 1-286 <HEN>
 beta-lactamase (BC 3.5.2.6) precursor - Escherichia
N;Alternate names: beta-lactamase TEM-6 (for blaT-6
C;Species: Bscherichia coli
C;Date: 30-Nov-1980 #sequence_revision 01-Sep-1981 #
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R;Sutcliffe, J.G. Symp. Quant. Biol. 43, 77-90, 1979 Cold Spring Harb. Symp. Quant. Biol. 43, 77-90, 1979 A;Title: Complete nucleotide sequence of the Escherichia A;Reference number: A90923; MUID:80002802; PMID:383387 A;Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Experimental source: PK2
R;Goussard, S.; Sougakoff, W.; Mabilat, C.; Bauernfeind, A.; Courvalin, P.
J. Gen. Microbiol. 137, 2681-2687, 1991
A;Title: An ISI-like element is responsible for high-level synthesis of extended-spectrum A;Reference number: S24415; MUID:92166702; PMID:1665171
A;Accession: S24415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 24-36, 'K', 38-286 < AMB>
A;Residues: 24-36, 'K', 38-286  
A;Experimental source: plasmid R6K
R;Kornacki, J.A.; Burlage, R.S.; Figurski, D.H.
J. Bacteriol. 172, 3040-3050, 1990
A;Title: The kil-kor regulon of broad-host-range plasmid A;Reference number: A35387; MUID:90264294; PMID:2160936
A;Accession: A35387
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R;Ambler, R.P.; Scott, G.K.
Proc. Natl. Acad. Sci. U.S.A. 75, 3732-3736, 1978
A;Title: Partial amino acid sequence of penicillinase coded by Escherichia coli plasmid A;Reference number: A93820; MUID:79012483; PMID:358199
A;Accession: A93820
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Proc. Natl. Acad. Sci. U.S.A. 75, 3737-3741, 1978
A;Title: Nucleotide sequence of the ampicillin resistance gene A;Reference number: A93821; MUID:79012484; PMID:358200
A;Accession: A93821
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C;Superfamily: Beta-lactamase I
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A;Residues: 1-101,'K',103-161,'H',163-286 <GOU>
A;Residues: 1-101,'K',103-161,'H',163-286 <GOU>
A;Cross-references: EMBL.X57972; NID:941816; PIDN:CAA41038.1;
A;Experimental source: ISI-like blaT-6 DNA
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A; Residues: 182-286 < KOR>
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A; Residues: 1-286 <SUT>
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QLIDWMEADK 213
                                                     QLIDWMEADK 190
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98.9%;
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Pred. No. 1.6e-79;
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A; Genome: plasmid
C; Superfamily: beta-lactamase I
C; Keywords: antibiotic resistance
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A;Title: A new example of physical linkage between Tn1 and Tn21: the antibiotic multiple A;Reference number: S30112; MUID:93062798; PMID:1331747
A;Accession: S30113
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A;Molecule type: DNA
A;Residues: 1-286 <RES>
A;Cross-references: EMBL:U21228; NID:g885956; PIDN:AAA70411.1; PID:g885958
C;Keywords: hydrolase
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Plasmid 29, 241-244, 1993
A;Title: Development of a native plasmid as a cloning vector A;Reference number: I40904; MUID:93361581; PMID:7689234
A;Accession: I40905
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A;Note: cloning vector pCG1408 engineered and expressed in Clavibacter xyli
C;Date: 15-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Oct-2000
C;Accession: I40905
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beta-lactamase (EC 3.5.2.6) - synthetic
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A; Residues: 1-286 < MAB>
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97.9%; Pred. No. 8.6e-79;
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R;Chanal, C.; Poupart, M.C.; Sirot, D.; Labia, R.; Sirot, J.; Cluzel, R. Antimicrob. Agents Chemother. 36, 1817-1820, 1992
A;Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase A;Reference number: S60310; MUID:93037315; PMID:1416873
A;Accession: S60310
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S60310
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A;Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes. A;Reference number: S60310; MUID:93037315; PMID:1416873
A;Accession: S60312
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C;Species: Klebsiella pneumoniae
C;Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 22-Jun-1999
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A; Residues: 1-286 < CHA>
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C;Superfamily: beta-lactamase
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A; Residues: 1-286 < CHA>
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                                                                                                                                            Similarity 97.4
85; Conservative
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AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                              HPETLVKVKDAEDKLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRVD
                                                                                 HPETLYKYKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60
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97.4%;
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97.4%;
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Pred. No. 2.4e-78;
3; Mismatches 2
                                                                                                                                          Score 956; DB 2
Pred. No. 3e-78;
3; Mismatches
                                                                                                                                                                                                                                                                                                         not shown
                                                                                                                                                                                  DB 2;
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C;Species: Sai
C;Date: 30-Sep
C;Accession: C
               A;Title: Complete nucleotide sequence and A;Reference number: JQ1538; MUID:92383313; A;Accession: JQ1546
                                                                                                                                                 Bla protein - Salmonella typhimurium plasmid
N;Alternate names: beta lactamase homolog
C;Species: Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Klebsiella pneumoniae C;Date: 12-Apr-1996 #sequence revision 19-Apr-1996 #text_change 09-Jul-2004 C;Accession: S60311; F37392; FQ0498 C;Accession: S60311; F37392; FQ0498 R;Chanal, C.; Poupart, M.C.; Sirot, D.; Labia, R.; Sirot, J.; Cluzel, R. Antimicrob. Agents Chemother. 36, 1817-1820, 1992 A;Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes. A;Reference number: S60310; MUID:93037315; PMID:1416873
                                                                         R; Cannon, P.M.; Strike, P. Plasmid 27, 220-230, 1992
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A; Residues: 1-32 < TOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Sequencing and expression of aadA, bla, and tnpR from A; Reference number: A37392; MUID:91172904; PMID:1963948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Tolmasky, M.E.
Plasmid 24, 218-226, 1990
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   A;Status: translation not shown
                                                                                                                                                                                                           JQ1546
                                                                                                                               ;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: GB:M55547; NID:g155010; PIDN:AAA98408.1; PID:g155016;
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                                                                                                                JQ1546
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97.4%;
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Pred. No. 3e-78;
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                                      gene organization; PMID:1325061
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A; Molecule type: DNA
A; Residues: 1-286 <CAN>
A; Cross-references: UNIPR
C; Genetics:
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                                                                                                                                                                                                                                                                                                                             A;Genome: plasmid
C;Superfamily: beta-lactamase I
C;Keywords: antibiotic resistano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Experimental source: plasmid pZMP1
R;Lee, K.Y.; Hopkins, J.D.; Syvanen, M.
J. Bacteriol. 172, 3229-3236, 1990
A;Title: Direct involvement of IS26 in an antibiotic resistance
A;Reference number: A35395; MUID:90264317; PMID:2160941
A;Accession: A35395
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S16146
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A;Residues: 1-30,'L',32-286 <LEE>
A;Residues: 1-30,'L',32-286 <IEE>
A;Cross-references: GB:X62115; NID:g48988; PIDN:CAA44025.1;
A;Experimental source: plasmid BWH77
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C; Superfamily:
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                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                               h 68.3%; Score 666; DB 2; I Similarity 66.7%; Pred. No. 3.1e-52; 26; Conservative 28; Mismatches 35;
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                                                                        GQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGFK 121
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                                                                                                                                                                 PETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRIDA 61
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ELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQQ 181
                                                                                                                                         PQPLEQIKQSESQLSGRVGMIEMDLASGRTLTAWRADERFPMMSTFKVVLCGAVLARVDA
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                                                  GDEQLERKIHYRQQDLVDYSPVSEKHLADGMTVGELCAAAITMSDNSAANLLLATVGGPA 142
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97.9%;
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Pred. No. 3e-78;
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beta-lactamase (EC 3.5.2.6) class A - Escherichia coli plasmid NAIternate names: beta-lactamase PIT-2; beta-lactamase SHV-1 C;Species: Escherichia coli C;Date: 31-Dec-1988 #sequence revision 31-Dec-1988 #text_change C;Accession: S00464 R;Barthelemy, M.; Peduzzi, J.; Labia, R. Biochem. J. 251, 73-79, 1988 Biochem. J. 251, 73-79, 1988 A;Reference number: S00464; MUID:88268817; PMID:3260490 A;Accession: S00464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Garbarg-Chenon, A.; Godard, V.; Labia, R.; Nicolas, J.C. Antimicrob. Agents Chemother. 34, 1444-1446, 1990
A;Title: Nucleotide sequence of SHV-2 beta-lactamase gene. A;Reference number: A60679; MUID:90351141; PMID:2201259
A;Accession: A60679
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C;Species: Salmonella typhimurium
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Aug-2004
C;Accession: A60679
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A; Residues: 1-286 < GAR>
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                                                                                                                   ;Genome: plasmid
;Superfamily: beta-lactamase I
                                                                                                                                                                            ,Molecule type: protein ,Residues: 1-265 <BAR>
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mes 126; Conserv
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                                                                                                antibiotic resistance; hydrolase
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LLQWMVDDR 211
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                    67.9%; Score 662; DB 2; 66.7%; Pred. No. 6.4e-52; ative 28; Mismatches 35;
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66.7%;
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Pred. No. 3.1e-52;
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A;Title: Nucleotide sequence and phylogeny of SHV-2 beta-lactamase A;Reference number: A44998; MUID:91136192; PMID:2285285
A;Accession: A44998
                                                                                                                                                                                                                                                     beta-lactamase (EC 3.5.2.6) SHV-2 - Klebsiella ozaenae plasmid pBP60 C;Species: Klebsiella ozaenae C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004 C;Accession: A44998; S12703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 1-265 < BAR>
C; Superfamily: beta-lactamase I
C; Keywords: antibiotic resistance; hydrolase
R;Podbielski, A.; Melzer, B.
Nucleic Acids Res. 18, 4916, 1990
A;Title: Nucleotide sequence of the gene encoding the SHV-2
A;Reference number: S12703; MUID:90370479; PMID:2395654
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A;Title: Single amino acid substitution between SHV-1 beta-lactamase
A;Reference number: S02434, MUID:88196385; PMID:3129309
A;Accession: S02434
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                                                                              A;Cross-references: UNIPROT:P14558; GB:M95179; NID:g150488;
                                                                                                                                       A;Status: preliminary
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11, 217-220, 1988
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Pred. No. 6.4e-52;
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                      (bla(SHV-2))
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A;Accession: S12703
A;Status: translation not shown
A;Acteus: type: DNA
A;Residues: 1-286 <POD>
A;Cross-references: EMBL:X53433; NID:943789; PIDN:CAA37524.1; PID:943790
C;Genetics:
A;Genome: plasmid
C;Superfamily: Beta-lactamase I
C;Keywords: antibiotic resistance; hydrolase
Query Match
Best Local Similarity 66.7%; Pred. No. 7.1e-52;
Matches 126; Conservative 28; Mismatches 35; Indels 0; Gaps 0;
Matches 126; Conservative 28; Mismatches 35; Indels 0; Gaps 0;
Matches 126; Conservative 28; Mismatches 35; Indels 0; Gaps 0;
Matches 126; Conservative 28; Mismatches 35; Indels 0; Gaps 0;
Matches 126; Conservative 28; Mismatches 35; Indels 0; Gaps 0;
Matches 126; Conservative 28; Mismatches 35; Indels 0; Gaps 0;
Matches 126; Conservative 28; Mismatches 35; Indels 0; Gaps 0;
Matches 126; Conservative 28; Mismatches 35; Indels 0; Gaps 0;
Matches 126; Conservative 28; Mismatches 35; Indels 0; Gaps 0;
Matches 126; Conservative 28; Mismatches 35; Indels 0; Gaps 0;
Matches 126; Conservative 28; Mismatches 35; Indels 0; Gaps 0;
Matches 126; Conservative 28; Mismatches 35; Indels 0; Gaps 0;
Matches 126; Conservative 28; Mismatches 35; Indels 0; Gaps 0;
Matches 126; Conservative 28; Mismatches 35; Indels 0; Gaps 0;
Matches 126; Conservative 28; Mismatches 35; Indels 0; Gaps 0;
Matches 126; Conservative 28; Mismatches 35; Indels 0; Gaps 0;
Matches 126; Conservative 28; Mismatches 35; Indels 0; Gaps 0;
Matches 126; Conservative 28; Mismatches 35; Indels 0; Gaps 0;
Matches 126; Conservative 28; Mismatches 35; Indels 0; Gaps 0;
Matches 126; Conservative 28; Mismatches 35; Indels 0; Gaps 0; Gaps 0;
Matches 126; Conservative 28; Mismatches 35; Indels 0; Gaps 0; Gap
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                 Database
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM protein - protein search, using sw model
  A Geneseq 16Dec04:*
1: geneseqp1990s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003ss:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-668-778-2_COPY_1_202
1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          June 10, 2005, 10:22:36; Search time 78.3206 Seconds (without alignments)
997.510 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                 2105692 seqs, 386760381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HPETLVKVKDAEDQLGARVG.....IDWMEADKVAGPLLRSALPA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
geneseqp1980s:*
geneseqp2000s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
۲ :	1032	100.0	263	٠.	AAE05544	Aae05544 E. coli m
N	1032		263	4	AAB36692	EBC
u	1032	8	263	œ	ADJ67709	_
4	1032	8	264	N	AAW16634	Aaw16634 Beta-lact
U	1032	100.0	264	N	AAW18680	_
თ	1032	100.0	286	N	AAR31575	
7	1032		286	N	AAR97619	Aar97619 Secretory
80	1032	100.0	286	N	AAR96423	
9	1032	100.0	286	N	AAW16635	
10	1032	100.0	286	N	AAW18679	Aaw18679 Secretory
11	1032	100.0	286	N	AAY08529	Aay08529 Vector pA
12	1032	100.0	286	w	AAB10442	Aab10442 Expressio
13	1032	100.0	286	ω	AAB10438	Aab10438 Expressio
14	1032	100.0	286	w	AAB10440	Aab10440 Expressio
15	1032	100.0	286	4	AAB50898	Aab50898 Protein e
16	1032	100.0	286	4	AAB31173	Aab31173 Amino aci
17	1032	100.0	286	S	AAU75551	Aau75551 celZ inte
18	1032	100.0	286	σ	ABP55474	Abp55474 Vector pC
19	1032	100.0	286	6	ABR43622	Cloning
20	1032	100.0	286	œ	ADR70422	Adr70422 Vector pA
21	1032	100.0	286	8	ADR70410	Adr70410 Vector pA
22	1032	100.0	286	8	ADR70404	Adr70404 Vector pA
23	1032	•	286	8	ADR70416	
24	1032	100.0	286	8	ADR70428	
25	1032	100.0	290	4	AAU23219	Aau23219 Novel hum

4.5	44	43	42	41	40	39	38	37	36	35	34	33	32	<u>3</u> 1	30	29	28	27	26
1027	1027	1027	1031	1031	1031	1031	1031	1032	1032	1032	1032	1032	1032	1032	1032	1032	1032	1032	1032
99.5	99.5	99.5	99.9	99.9	99.9	99.9	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
265	265	265	1967	1293	1293	872	286	2761	2307	2307	2307	1277	1088	1031	585	408	327	327	290
N	N	N	6	7	7	7	N	N	w	ω	w	N	N	ഗ	σ	σ	N	N	4
AAW48613	AAY08232	AAY08234	ABB82793	ADH14284	ADC22811	ADK65686	AAY06551	ADH11249	AAY70066	AAY70065	AAY70064	AAR52701	AAR88636	ADI46109	ADA67747	ABR55981	AAW18681	AAW16636	AAM84362
Aaw48613	Aay08232	Aay08234	Abb82793	Adh14284	Adc22811	Adk65686	Aay06551	Adh11249	Aay70066	Aay70065	Aay70064	Aar52701	Aar88636	Adi46109	Ada67747	Abr55981	Aaw18681	Aaw16636	Aam84362
Escherich	E. coli F	[75] •	Amino aci	Vector po	Human G p	E coli cl	Escherich	Vertebrat	Recombina	Recombina	Recombina	Plasmid		Single st	Beta-lact	hCG beta-	Membrane	Beta-lact	Human 1mm

ALIGNMENTS.

AAE05544 standard; protein; 263 ₽

AAE05544;

24-SEP-2001 (first entry)

E. coli mature TEM-1 beta-lactamase.

RESULT 1
AAE05544
ID AAE0
XX AAE0
AC AAE0
XX AAE0
XX INC
DT 24-S
XX INC
CX INC Interaction-dependent enzyme association; IdEA system; biosensor; circularly permutated interaction-activated protein; marker protein; type A beta-lactamase; TEM-1 beta-lactamase; protein-protein interaction; therapeutic; drug screening; thioredoxin; ampicillin resistance.

Escherichia coli.

P P	Key Cleavage-site	Location/Qualifiers 2728
F F	Region	<pre>/note= "Break-point between alpha and omega fragments" 3640</pre>
H.	9	/note= "Inter-sub-domain loop"
FΤ	Cleavage-site	3839
FΤ	,	<pre>/note= "Break-point between alpha and omega fragments"</pre>
FΤ	Active-site	45
ΕŢ	Cleavage-site	7475
Ŧ		<pre>/note= "Break-point between alpha and omega fragments"</pre>
FΤ	Cleavage-site	149150
ΨŢ		<pre>/note= "Break-point between alpha and omega fragments"</pre>
FΤ	Cleavage-site	172173
FT		<pre>/note= "Break-point between alpha and omega fragments"</pre>
Ŧ	Region	189204
FΤ		/note= "Inter-sub-domain loop"
FΤ	Cleavage-site	190191
FΤ		<pre>/note= "Break-point between alpha and omega fragments"</pre>
ΕŢ	Cleavage-site	202203
FΤ		<pre>/note= "Break-point between alpha and omega fragments"</pre>
Ţ	Cleavage-site	228229
FΤ		<pre>/note= "Break-point between alpha and omega fragments"</pre>
X		
PN	WO200151629-A2.	
×		
B	19-JUL-2001.	
×		

16-JAN-2001; 2001WO-US001651.

X # X 13-JAN-2000; 2000US-0175968P. 15-MAR-2000; 2000US-00526106.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The systems are also useful in selecting with a single marker protein the cincorporation of multiple genetic traits in a host cell. In particular, the systems are useful in many applications in human therapeutics, consists and prognostics, as well as in high-throughput screening consists and prognostics, as well as in high-throughput screening consists for the discovery and validation of pharmaceutical targets and converse of the converse of the converse of the converse of two-ful systems (e.g. E. coli Dimer Detection System, yeast two-ful the converse of the coli pimer Detection System, yeast two-ful the converse of the coli pimer betection System, yeast two-ful the coli daystem of simultaneous detection of multiple interactions between converse of simultaneous detection of multiple interactions between converse of the circularly permutated marker proteins in a high throughput format. The circularly permutated marker proteins comprising interaction-converse of the converse of cells, the converse of the colimpath of pair-wise protein pathways, in high-converse of pair-wise protein pathways, in high-colimpath protein interaction. The present sequence is Escherichia colimpate and colimpate of the collimpate of the protein interaction. The present sequence is Escherichia colimpate of the collimpate of the protein interaction of any collimpate of the collimpate 
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IdEA) systems that comprise a fusion sequence that encodes for a circularly permutated, interaction-activated proteins that reassemble to form functionally reconstituted marker proteins which produce a detectable signal upon the association of two oligopeptides, or upon simultaneous association of two oligopeptides with a third oligopeptide. The marker protein is preferably a type A beta-lactamase, especially TEM-1 beta-lactamase of Escherichia coli. The oligopeptide is a member of a proteome library selected from single chain antibody Fv fragment library, an antibody light chain variable region library and a peptide library displayed within thioredoxin. The IdEA systems are useful for detecting and identifying interactions between intracellular as well as extracellular proteins, particularly between two or three polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interaction-dependent enzyme association systems for detecting interactions between two or three polypeptides, especially in human therapeutics, diagnostics or prognostics, comprise circularly permutated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 38; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-451857/48.
N-PSDB; AAD10411.
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181
                                              181
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                                                                                                                                                                                                         61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                             HPETLYKYKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60
                                                                                                                                   KELTAFLHNMGDHVTRLDRWEPEINEAIPNDERDTTMPVAMATTLRKLLITGELLTLASRQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 AA;
QLIDWMEADKVAGPLLRSALPA
                                        QLIDWMEADKVAGPLLRSALPA
                                                                                                  KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMFVAMATTLRKLLTGELLTLASRQ 180
                                                                                                                                                                                                         AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                                                                                                                                                           AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                                                                                                                                                                                                                                 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1032; DB 4;
Pred. No. 1.5e-103;
                                                 202
                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                            RESULT 2
AAB36692
                                                                                                                                                                                                                                                                                   The present invention describes a fragment complementation system (I) CC which comprises a first oligopeptide (OP1) containing an N-terminal CC fragment with a C-terminal break point and a second oligopeptide (OP2) CC comprising a C-terminal with a N-terminal breakpoint, in which the C and CC reassemble to form a functionally reconstituted MP. Methods from the CC present invention are used for monitoring the occurrence of protein (MP) and CC protein interactions in a sample, identifying oligopeptide interactions CC between two different proteomes, identifying epitopes that bind to an CC immunoglobulin (Ig) variable region, for identifying interactions between CC an extracellular domain of a transmembrane protein and a polypeptide, for CC injunted signal transducers, forming a maryme complementation system for cegulated signal transducers, forming a enzyme complementation system for CC selecting simultaneous incorporation of multiple genetic elements into a host who is in need of it. The present sequence represents CC the Escherichia coli mature TEM-1 beta-lactamase, which is used in the CX compound in a host who is in need of it. The present sused in the
                                                                                                                                                                                          Matches
                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel fragment complementation system to identify interactions between polypeptides comprises fragment pairs having first and second members that reassemble into a marker protein which has a directly detectable
                                                                                                                                                                                                                                                          Sequence 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAC90773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAY-1999; 99US-0135926P.
13-JAN-2000; 2000US-0175968P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAR-2000; 2000WO-US007108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interaction-activated protein; beta-lactamase; protein interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli mature TEM-1 beta-lactamase protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB36692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB36692 standard; protein; 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-032034/04.
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                121
                                                                                                                                                                                          202;
                                                  61
                                                                                  51
                                                                                                                                                                                                            Similarity
XELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTIMPVAMATTLRKLLTGELLTLASRQ 180
                                                                       AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                                        HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                                                  AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                      HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fig 2; 94pp; English.
                                                                                                                                                                                                                                                            AA;
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                                                                                                                                                                                                        100.0%;
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                                                                                                                                                                                                      Score 1032; DB 4;
Pred. No. 1.5e-103;
                                                                                                                                                                                          Mismatches
                                                                                                                                                                                          0,
                                                                                                                                                                                                                        Length 263;
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The invention describes a fragment complementation system (I) comprising CC a first oligopeptide having an N-terminal fragment with a C-terminal CC break-point, and a second oligopeptide having a C-terminal fragment with CC a N-terminal break-point, where the N-terminal fragment and the C-CC terminal fragment each are derived from a marker protein and reassemble CC to form a functionally reconstituted marker protein. (I) is useful for CC selecting simultaneous incorporation of multiple genetic elements into a CC compound in a host. The method described is useful for identifying a CC second oligopeptide to which a first oligopeptide binds, involving co-CC expressing the first and second oligopeptides. Binding of the first CC compound the cocurrence of protein. The method is also useful for CC identifying oligopeptide interactions in the functional CC reassembly of the marker protein. The method is also useful for CC identifying oligopeptide interactions between two different proteomes; CC identifying oligopeptide interactions between two different proteomes; CC identifying epitopes that bind to an immunoglobulin variable region. CC (I) or an expression casette (II), encoding a selectable N or C-terminal CC domain of a transmembrane protein and a polypeptide, where the CC transmembrane protein is an immune cell protein, perferably CD40. (I) or inhibit phosphorylation-regulated cell signal transducers. (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fragment complementation system; marker protein; multiple genetic element incorporation; antibiotic resistance; beta-lactam derivative activation; anti-tumour compound; functional reassembly; protein-protein interaction; proteome immunoglobulin variable region; immune cell protein; CD40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fragment complementation system for detecting immunoglobulin epitope, has first oligopeptide containing N-terminal fragment with C-terminal break-point, second oligopeptide containing C-terminal fragment with N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2004038317-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAY-1999;
13-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-FEB-2004.
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DB; ADJ67708.
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99US-0135926P.
2000US-0175968P.
2000US-00526106.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 263
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                                                                                                                                                                    Molecular chimaera for gene or virus directed enzyme prodrug therapy useful for treatment of cancer, viral infection or inflammation.
                                                                                                                                                                                                                                                                       ; IAM
                                                                                                                                                                                                                                                                                                                  Dev I,
                                                                                                                                                                                                                                                                                                                                                                                                                   20-NOV-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene directed enzyme prodrug therapy; GDEPT; virus directed enzyme prodrug therapy; VDEPT; beta-lactamase; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beta-lactamase (including signal peptide).
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                                                                                                                                                                                                                                                                                                                                                                  GROUP LTD
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/label= Sig_peptide
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L.5e-103;
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chat can be
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Escherichia coli beta-lactamase (AAW16634), including the signal peptide, is the expression product of a molecular chimaera, designated pCMV-BL (AAT66737), in which the beta-lactamase gene is under control of the CMV intermediate/early promoter. Vectors consisting of a transcriptional

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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                regulatory DNA sequence linked to a beta-lactamase gene can be used for enzyme prodrug therapy. Expression of the beta-lactamase in a targetted cell allows conversion of a prodrug into an agent toxic to the cell for treatment of cancer, viral (e.g. HIV) infection or inflammation.

Secretion of the enzyme has the advantage of increasing neighbouring center.
 The intracellular form (AAW18680) of TEM beta-lactamase is expressed by pCMV-delBL (AAT70311) in which a PCR-amplified beta-lactamase coding sequence, minus the signal sequence, is placed under control of the intermediate/early promoter of cytomegalovirus. Intracellular beta-lactamase constructs, placed under control of promoter/enhancer elements of lung-associated protein or neuroendocrine marker protein genes, can be
                                                                                                                                     DNA construct for gene-directed enzyme prodrug therapy of lung cancer comprises lung- or neuroendocrine-specific promoter controlling
                                                                                                                                                                                                                                                                                                                                                      WO9719183-A2
                                                                                                                                                                                                                                                                                                                                                                               Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                    Prodrug therapy; gene directed enzyme prodrug therapy; GDEPT; virus directed enzyme prodrug therapy; VDEPT; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                      20-NOV-1995;
                                                                                                                                                                                                                                                                                                 19-NOV-1996;
                                                                                                                                                                                                                                                                                                                             29-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW18680 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Intracellularly-expressed beta-lactamase.
                                                                                                                                                                                                                                             (GLAX )
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DB; AAT70311.
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                                                                                                                                                                                                                                             GLAXO
                                                                                                                                                                                                                   Moore
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGQEQLGRRIHYSQNDLVEYSPVTBKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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The expression constructs pRNH127 and pRNH155 contain identical sequences but were constructed using different strategies (see AAQ36498). The constructs comprise exons 2-7 of human CYP1A1 gene under the control of the inducible mouse metallothionein (MMT-1) promoter. The constructs also contain an open reading frame in the opposite orientation to the cytochrome P450 exons. This ORF encodes ampicillin resistance. The constructs are suitable for transformation of human fibroblasts derived from the xeroderma pigmentosum group A. Cultures of the transformed fibroblasts can be used to test substances for mutagenicity. The presence

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RESULT 7
AAR97619
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pCMV-BL (AAT29220), in which the beta-lactamase coding sequence is under the control of the intermediate/early cytomegalovirus promoter. Beta-lactamase delivery to mammalian cells confers sensitivity to cephalosporin prodrugs. Liposomal DNA/5-fluorouracil prodrug combinations resulted in s.c. tumour regression in mice bearing A549 tumours. Survival of mice bearing human large cell lung H460 intrathoracic (i.t.) tumours was increased upon i.t. injection of the secretory beta-lactamase DNA
                                                                                                                                                                                                                                                                                                                              Molecular chimaera for use in enzyme gene therapy - is activated in target cell to express a secretable enzyme which cleaves a prodrug outside the cell into a cytotoxic or cytostatic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene therapy; gene directed enzyme prodrug therapy; GDEPT; virus directed enzyme prodrug therapy; VDEPT; prodrug activation; cytotoxic; cytostatic; cancer; tumour; retrovirus; vector;
                                                                                                                                                                                                                                                                      Example 3; Page 57-58; 73pp; English.
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                                                                                                                                                                                                                 A secretory beta-lactamase (AAR97619) is expressed from DNA construct
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Pred. No. 1.7e-103;
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                                                                                                                                                                                                                                                                                                      Testing chemicals for cytotoxicity to human by using recombinant fibroblasts transformed with control of inducible promoter.
                                                                                                                                                                                                                                                            Disclosure; Col 17-24; 26pp; English.
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09-DEC-1992;
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(first entry)
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92US-00990295.
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The present sequence is encoded by a chimeric mouse metallothionein-cytochrome P450IA1 (CYPIA1) expression construct. Two clones, pRNH127 and pRNH15, were isolated by different methods and which both had the same sequence. The CYPIA1 construct is used in assays to test for cytotoxicity of humans to a chemical. The method comprises exposing human fibroblast cells normally not including any cytochrome P450 activity to potentially toxic chemicals. The cells having been transforme to express cytochrome P450, under the control of a controllable promoter through the CYPIA1 gene, upon exposure to the chemical in vitro. The chemical is metabolised intracellularly into a cytochrome metabolite by oxidation within the

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RESULT 9
AAM16635
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Best Local S
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                                  Escherichia coli beta-lactamase (AAW16635), lacking the signal peptide, is the expression product of a molecular chimaera, designated pCMV-delBL (AAT66738), in which the beta-lactamase gene is under control of the CMV intermediate/early promoter. Vectors consisting of a transcriptional regulatory DNA sequence linked to a beta-lactamase gene can be used for enzyme prodrug therapy. Intracellular expression of the beta-lactamase in a targetted cell allows conversion of a prodrug into an agent toxic to the cell for treatment of cancer, viral (e.g. HIV) infection or
                                                                                                                                                                                                                                                                        Example;
                                                                                                                                                                                                                                                                                                                          Molecular chimaera for gene or virus directed enzyme prodrug therapy useful for treatment of cancer, viral infection or inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-NOV-1996;
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Pred. No. 1.7e-103;
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               BL (AMT70309) in which a PCR-amplified beta-lactamase coding sequer placed under control of the intermediate-dearly promoter of cytomegalovirus. Secretory beta-lactamase constructs, placed under control of promoter/enhancer elements of lung- associated protein of the control of promoter and the control of pro
                                                                                                   The secreted form (AAW18679) of TEM beta-lactamase
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This invention describes a novel tetracycline assay that uses recombinant prokaryotic cells comprising a luciferase gene under the transcriptional control of a tetracycline repressor and tetracycline promoter and involves the detection of luminescence emitted form the cells. The assay can be used to distinguish tetracycline form other microbial agents. The invention also describes a novel plasmid comprising either the luxCDABE genes, a tetracycline repressor (TetA) and a tetracycline promoter (TetA) and a tetracycline repressor (tetR) and a tetracycline assay and a tetracycline promoter (TetA) from Tn10. The tetracycline assay method can be used for the determination of tetracycline in a sample,
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Pred. No. 1.7e-103;
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                                                                                                                  Selecting monoclonal antibodies, by expl
hybridomas attached to antibody-binding
                                                                                                                                                                                             Breitling F,
                                                                                                                                                                                                                                                                          11-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                Expression vector; antibody binding protein; monoclonal antibody; Neo-R; B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.
                                                                                                                                                                                                                                                                                                                                                                                                                         Expression vector
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Pred. No. 1.7e-103;
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This invention describes a novel method for the selection of monoclonal antibodies (MAb) which comprises (i) fusing B lymphocytes with myeloma cells to produce antibody-producing hybridomas such that the antibodies are presented at the surface of the hybridomas by an antibody-binding protein (I); and (ii) binding the antibody to antigens (Ag). The

Claim 16;

Fig 3; 22pp; German.

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                                                                                                                                         Selecting monoclonal antibodies, by expressing them on the surface hybridomas attached to antibody-binding protein, then reaction with antibody library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DE19900635-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expression vector; antibody binding protein; monoclonal antibody; Neo-R; B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB10438
                                                                Claim 16; Fig 1; 22pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                       Breitling F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JAN-1999;
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)B; AAA71428.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expression vector pSEX11G2 bla protein
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                                                                  N-PSDB; AAA71429.
                                                                                                     WPI; 2000-499832/45.
                                                                                                                                                                 Breitling F,
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Selecting monoclonal antibodies, by expressing them on the

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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                    bla resistance marker; recombinant host cell; saccharification; fermentation; polysaccharase; oligosaccharide degradation; celZ gene; glucanase; integration vector; pLO12306.
                                                                                                                                                              26-MAY-2000;
                                                                                                                                                                                                                                 30-NOV-2000
                                                                                                                                                                                                                                                                                                                                                              Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein encoded by bla resistance marker of integration vector pLO12306.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB50898 standard; protein; 286 AA
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                                                                                                 26-MAY-1999;
                                                                                                                                                                                                                                                                                              WO200071729-A2
                                 (UYFL ) UNIV FLORIDA RES FOUND
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ilarity 100.0%;
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Pred. No. 1.7e-103;
D; Mismatches 0;
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Search completed: 0 Job time: 79.3206

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  control of a surrogate promoter capable of increasing expression of the polysaccharase. The host cell also contains a second heterologous polynucleotide encoding a secretory polypeptide to facilitate the secretion of the expressed polysaccharase. The recombinant host cell is useful for producing polysaccharase which is useful for enzymatically degrading oligosaccharides such as lignocellulose, hemicellulose, cellulose, pectin or their combinations, and fermenting the product to ethanol, by simultaneous saccharification and fermentation processes. The present sequence is encoded by an integration vector which was introduced into cells to generate recombinant host cells. The vector contains a surrogate promoter from Zymomonas mobilis, the celz gene from Erwinia chrysanthemi, resistance markers bla and tet, and Klebsiella oxytoca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is given in a specification relating to a recombinant host cell suitable for simultaneous saccharification are fermentation. The host cell contains at least one heterologous polynucleotide encoding a polysaccharase under the transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 286 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     target sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant host cells useful for producing polysaccharase for degrading oligosaccharides, comprises a first heterologous polynucleotide encoding polysaccharase under control of surrogate promoter.
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tive 0; Mismatches 0;
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Result
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Perfect score:
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-490-153-265
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Qy 1 HPETLYKYKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRI	Query Match 100.0%; Score 1032; Best Local Similarity 100.0%; Pred. No. 1 Matches 202; Conservative 0; Mismatche	1	FILING DATE: 19910627 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Kohn, Kenneth I. REGISTRATION UNMBER: 9-321 REFERENCE/DOCKET NUMBER: P-321 TELECOMMUNICATION INFORMATION:	g 8	ADDRESSEE: I STREET: P.O CITY: Troy	IL NO. 5180666 ERAL INFORMATION: PPLICANT: States, J. Christopher PPLICANT: Hines, Ronald N. PPLICANT: NO. 5180666ak, Raymond F. PPLICANT: NO. 5180666ak, Raymond F. ITLE OF INVENTION: METHOD AND CELL LI ITLE OF INVENTION: MUTAGENICITY OF A MBER OF SEQUENCES: 2 PRESSONNEY ENDRESS:	ALIGNMENTS RESULT 1 US-07-721-775A-2	.0 2307 .0 2307 .0 2307 .0 2307 .9 286 .9 1293 .9 1293 .9 1293 .9 1293 .9 1293	1032 100.0 299 4 US-09-490. 1032 100.0 2307 3 US-09-263. 1032 100.0 2307 3 US-09-263. 1032 100.0 2307 4 US-09-919. 1032 100.0 2307 4 US-09-919.
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,658
FILING DATE: 15-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,295
FILING DATE: 09-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
DEFEDENCE /DCYFT NUMBER: D-721WSII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (313) 689-4071 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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APPLICANT: Hines, Ronald N.
APPLICANT: No. 5525482ak, Raymond F.
TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 689-3554
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Reising, Ethington, Barnard, Perry & Milton
STREET: P.O. Box 4390
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TOPOLOGY: linear
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CITY: Troy
STATE: Michigan
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KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 203
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Pred. No. 1.6e-113;
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RESULT 4
US-09-263-933-14
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; ORGANISM: Artificial Sequence US-09-263-933-14
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SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 7
                                                                                                             GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jockson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta Gene System for USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
                                                                                              SEQ ID NO 14
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Best Local Similarity
Matches 202; Conserv
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                                            LENGTH: 28
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
FEARLIER APPLICATION UNMBER: 09/129,611
FEARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
US-09-263-933-21
                                                                                                                           US-09-025-769B-265
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                                                              Sequence 265, Application US/09025769B Patent No. 6300064 GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Pottes, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
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Best Local Similarity
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Best Local Similarity
                       APPLICANT:
      PPLICANT:
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US-09-025-769B-362
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Best Local S
Matches 202
                                                                                                                                                                                                             Patent No.
                   GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
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FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO:
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TOPOLOGY: lines-
WOLECUTE
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ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
    CORRESPONDENCE ADDRESS
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
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5. 6300064
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100.0%; Pred. No. 1.6e-113;
tive 0; Mismatches 0;
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Gaps

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143

203

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York STATE: New York

USA

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APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jatkson, Roberta L.
APPLICANT: Patick, May K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR FILING DATE: 1999-08-05
NUMBER OF SEQ ID NOS: 33
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 7
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PRIOR APPLICATION UNMER: BP 95
PRIOR APPLICATION UNMER: BP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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LENGTH: 286 amino acids
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; OTHER INFORMATION: :
US-09-919-901-14
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US-09-919-901-14
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SEQ ID NO 14
LENGTH: 286
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                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                      Query Match
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APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REFORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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QLIDWMEADKVAGPLLRSALPA 202
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100.0%; Pred. No. 1.6e-113;
tive 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 21
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US-09-490-070A-265
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US-09-919-901-21
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Patent No. 6696248
GENERAL INFORMATION:
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APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: :
                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe
                                                                                                                                                                                                  Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Knappik, Achim
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                                                                      STREET: 1666 K Street, N.W., Suite 300 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QLIDWMEADKVAGPLIRSALPA 225
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                                                 COUNTRY: USA
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                               20006
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Ilag, Vic
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                                                                                                                                                                                                                                                                      Simon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 6696248
GENERAL INFORMATION:
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Best Local Similarity 100.0%;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION UNMER: EP 95 11 3021.0
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
APPLICATION NUMBER: EP 95 11 3021.0
APPLICATION NUMBER: 31,298
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELEPHONE: (202) 912-2000
TELEPHONE: (202) 912-2020
COMPUTER REALABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                      Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSES: COlin G. Sandercock, Esq. c.
White & MCAuliffe
White & MCAuliffe
CITY: Washington
STATE: D.C.
STATE: D.C.
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Knappik, Achim
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Ilag, Vic
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Pred. No. 1.6e-113;
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US-09-490-153-265
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GENERAL INFORMATION:
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Best Local Similarity
Matches 202; Conserv
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ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,153

FILING DATE: 24-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                         Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 24-Jan-2000 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
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                       PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                      STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                 STREET: 1251 Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 203
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APPLICATION NUMBER: US/09/025,769B
                                                                                                                                                                                                                                   ZIP: 1002:
                                                                                                                                                                                                                                                                                                                      ADDRESSEE: James F. Haley, Jr., Esq. STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/490,070A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09490153
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TOPOLOGY: linear

HOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-490-153-265
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US-09-490-153-362
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GENERAL INFORMATION:
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Best Local Similarity
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION NUMBER: US/09/490,153

FILING DATE: 24-Jan-2000

PRIOR APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-PEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSES: James F. Haley, Jr., Esq.
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
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APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84
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REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (212)596-9090
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Pred. No. 1.6e-113;
); Mismatches 0;
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APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

ITILE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/10/191,966

CURRENT FILING DATE: 2002-07-10

PRIOR APPLICATION NUMBER: US/99/263,933

PRIOR APPLICATION NUMBER: US/99/263,933

PRIOR APPLICATION NUMBER: US/99/263,933

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR FILING DATE: 1998-08-05

NUMBER: OF SEQ ID NOS: 33

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 7

LENGTH: 786
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OTHER INFORMATION: :
US-10-191-966-7
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Best Local Similarity
Matches 202; Conserv
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                                                                                                                                                                                                                                                                                                                        LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
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INFORMATION FOR SEQ ID NO: 362:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 362:
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REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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61 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGF 120
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                                                                            1 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60
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06wwy4 hafnia alve
06wwy4 hafnia alve
06wwy8 escherichia
06wb67 hordeum vul
038058 bacteriopha
000626 staphylococ
079c16 methylobaci
079dr3 sescherichia
084h50 escherichia
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Q5-JUL-2004 (TrEMBLrel. 27,
Q5-JUL-2004 (TrEMBLrel. 27,
Beta-lactamase (Fragment).
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PRINTS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA LACTAMASE_A; 1.
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SEQUENCE 229 AA; 25067 MW; C85582C
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Submitted (APR-2004) to the
EMBL; AY265885; AAP93843.1;
HSSP; P00807; 1KGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klebsiella oxytoca.
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Klebsiella.
NCBI_TaxID=571;
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                                                                                                                                                                                                                                                                                                KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ
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                                                                              PRELIMINARY;
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Last seq
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q6W9J1
Q6WZD4
Q6WZD4
Q6WZD4
Q7B3X5
Q7B899
Q7B875
Q7BR75
Q7DFY3
Q7DFD3
Q7DHD3
Q7DHD3
Q844X1
Q844X1
Q86485
Q987770
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Pred. No. 1.3e-77;
; Mismatches 0;
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Q6wzcd4
Q7b3x56
Q7b899
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Q7bf73
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Query Match
Best Local :
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Obert C.A., Goldstone C.M., Gordon D.M.,
Submitted (Apr.2004) to the EMBL/GenBank/
EMBL; AY265886; AAP93844.1; -.
HSSP; P00807; IKGE.
InterPro; IPR000871; Beta lactamase A.
PRINTS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA LACTAMASE A; 1.
                                                                                                                                                                STRAIN=MISC112;
Obert C.A., Goldstone C.M., Gordon D.M.,
Submitted (Apr-2004) to the EMBL/GenBank,
EMBL; AY265882; AAP93840.1; -.
HSSP; P00807; 1KGE.
InterPro; IPR001466; Beta lactamase.
InterPro; IPR001469; Beta_lactamase_A.
Pfam; PF00144; Beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
PRINTS; PR00118; BLACTAMASEA.
                                                                    NON TER
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SEQUENCE
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06WWY8;

05-JUL-2004 (TremBLrel. 27,

05-JUL-2004 (TremBLrel. 27,

05-JUL-2004 (TremBLrel. 27,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beta-lactamase (Fragment).
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                                                                                                                                              PROSITE; PS00146;
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=573;
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                                                                       241
241 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232 AA;
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                                                                                                                                            BETA_LACTAMASE_A; 1.
                                                                       241
26407 MW;
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100.0%;
100.0%;
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Last annotation update)
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EMBL/GenBank/DDBJ databases.
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Score 1032; DB 2;
Pred. No. 1.4e-77;
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                                                                         38DF2AFDF0C5807D CRC64;
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                                                                                                                                                                                                                                                                                                                                             Riley M.A.;
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                                                                                                                                                                                                                                                                                                                         databases.
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Q6KB67;
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O6WWY3 PRELIMINARY; PRT; 242 AA.
O5-JUL-2004 (TrEMBLrel. 27, Created)
O5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
O5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00146; BETA_LACTAMASE_A;
NON_TER 1 1
NON_TER 242 242
SEQUENCE 242 AA; 26554 MW; 38C3I
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InterPro; IPR00871; Beta_lactamase_A.
Pfam; PF00144; Beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
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HSSP; P00807; 1KGE.
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Name=blaTEM;
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                                                                                                                                                                                                                                                                                                                                                  AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242
26554 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1032; DB 2;
100.0%; Pred. No. 1.4e-77;
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Best Local Sim:
Matches 202;
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Jansen C., Korell M., Eckey C., Biedenkopf D., Kogel K.H.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ717739; CAG30723.1; -.
HSSP; P00807; 1ALQ.
InterPro; IPR001466; Beta_lactamase.
InterPro; IPR001466; Beta_lactamase.
InterPro; IPR00147; Beta_lactamase_A.
Pfam; PF00144; Beta-lactamase; 1.
Print; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE_A; 1.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein (Fragment).
Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magmoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDILINE=95172401; PubMed=7867948; DOI=10.1016/0378-1119(94)00839-K;

Henrich B., Schmidtberger B.;

"A variant of phiX174 gene E-based positive selection vectors with
enhanced lytic potential.";

Gene 154:51-54(1995).
                   EMBL; Z35638; CAA84692.1; -.
PIR; S47061; S47061.
HSSP; Q9R435; 1HTZ.
InterPro; IPR001466; Beta_lactamase.
InterPro; IPR000971; Beta_lactamase_A.
Pfam; PF00144; Beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
                                                                                                                                                                                                                                                                                                                                                                                        Bacteriophage phi-X174.
Viruses; ssDNA viruses; Microviridae;
NCBI_TaxID=10847;
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01-NOV-1996
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285 AA;
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Last annotation updat
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Best Local S
Matches 202
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Best Local Similarity
Matches 202; Conserv
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Q00626 O08022; O08102; O09393; O09396; O09397; O09398;
O09400, O09401; O09402; O09403; O09404, O09405; O09406;
O09408; O09481; O09482; O09483; O09490; Q57339;
O1-NOV-1996 (TYEMBLTel. 01, Created)
O1-NOV-1996 (TYEMBLTel. 01, Last sequence update)
25-OCT-2004 (TYEMBLTel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                         EMBL; U36912; AAB39957.1; -.
EMBL; U36911; AAB39956.1; -.
EMBL; U36911; AAB39956.1; -.
InterPro; IPR00146; Beta_lactamase.
InterPro; IPR000871; Beta_lactamase_A.
Pfam; PF00144; Beta-lactamase; 1.
                                                                                                                                                                                                                                                                                                                                                                                           PLĀSMID=J3356/pOX7/3, and J3356/POX7/1;
MEDLINE=96422755; PubMed=8825372; DOI=10.1006/plas.1995.0005;
Needham C., Noble W.C., Dyke K.G.;
"The staphylococcal insertion sequence IS257 is active.";
Plasmid 34:198-205(1995).
                                                                                                                                                                                                                                                                                                PRINTS; PRO0118; BLACTAMASEA
PROSITE; PS00146; BETA_LACTAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus.
Plasmid J3356/pOX7/1.
Plasmid J3356/pOX7/3, and Plasmid J3356/POX7/1.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
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Pred. No. 1.7e-77;
; Mismatches 0;
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Best Local Similarity
Matches 202; Conser
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Q79DR3
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Q79CL6;
05-JUL-2004
                                                                                                                                                                                                                                           Mutant extended-spectrum beta-
Name=bla; Synonyms=blaTEM-116;
Escherichia coli.
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MEDLINE=97074643; PubMed=8917070; DOI=10.1016/0378-1119(96)00114-X; Serebrijski I.G., Vassin V.M., Tsygankov Y.D.;

"Two new members of the BioB superfamily: cloning, sequencing and expression of bioB genes of Methylobacillus flagellatum and Corynobacterium glutamicum.";

Gene 175:15-22(1996).
                                                                                                                                      Plasmid pRP4, and Plasmid pCAPs.
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q79DR3
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InterPro; IPR000871; Beta_lactamase_A.
Pfam; PF00144; Beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE A; 1.
PROSITE; PS00146; BETA_LACTAMASE A; 1.
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Submitted (JUL-1995) to the
EMBL; U31280; AAC44581.1;
HSSP; P00807; IALQ.
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                                                                                                 NCBI_TaxID=562;
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e EMBL/GenBank/DDBJ databases.
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Pred. No. 1.7e-77;
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Best Local
            Q38212;
Q38212;
01-NOV-1996
01-NOV-1996
01-MAR-2002
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"Molecular Characterization of Extended-Spectrum Beta-Lactamases produced by Clinical Isolates of Klebsiella pneumoniae and Escher coli from a Korean Nationwide Survey.";

J. Clin. Microbiol. 42:2902-2905 (2004).

EMBL; W74750; AAA24057.1; -.

EMBL; W12598; AAA24057.1; -.

EMBL; AV42598; AAA25605.1; -.

EMBL; AV42598; AAA25605.1; -.

EMBL; AV42598; AAA25605.1; -.
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 Bacteriophage
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SIGNAL 1
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PROSITE; PS00146; BETA_LACTAMASE_A;
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Rondot S., Anthony K., Dubel S., Ida N., Beyre
Little M., Breitling F.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ
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Escherichia coli.";
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Submitted (AUG-1991) to the EMBL/GenBank/DDBJ databases
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(TrEMBLrel. 01, Last sequence update)
(TREMBLrel. 20, Last annotation update)
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Query Match
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Best Local Similarity
                                                                                                                                                                Ghandili S., Hosseini-Mazinani S.M.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ dat
EMBL; AY583761; AAS86427.1; -.
HSSP; P00807; 1ALQ.
InterPro; IPR001466; Beta_lactamase.
InterPro; IPR001466; Beta_lactamase.
InterPro; IPR00181; Beta_lactamase, 1.
PAGNITS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE_A; 1.
PROSITE; PS00146; BETA_LACTAMASE_A; 1.
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Topal M.D., Badie J.S., Conrad M.;
Topal M.D., Badie J.S., Conrad M.;
"O-6-methylguanine mutation and repair is nonuniform: Selection
DNA most interactive with O-6-methylguanine.";
DNA most interactive with O-6-methylguanine.";
J. Biol. Chem. 261:9879-9885(1986).
EMBL; M14017; AAA32208.1;
EMBL; M14017; AAA32208.1;
HSSP; Q9R435; 1HTZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Inhibitor-resistant TEM beta-lactamase (Fragment).
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NON_TER 1 1
SEQUENCE 225 AA; 25022 MW; 009BF84
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Viruses; ssDNA viruses;
                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=U33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Escherichia.
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232 AA;
  Conservative
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25558 MW;
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                        99.5%;
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Score 1027; DB 2; Length 232; Pred. No. 3.4e-77; 1; Mismatches 1; Indels
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                                                                                                     5791CD285EE70BB0
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RESULT 13
Q84H49
Q84H4
AC Q84H4
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-OC
DE TEM-1
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Q8445
ID Q8445
AC Q8445
DT 01-UU
DT 01-OC
DB TEM-1
OC Bacte
OC Bacte
OC CITE
CO NCBL
RA BOX A
RL SUDMI
DR SEQUE
RA BOX A
RL SUDMI
DR HSSP;
DR Intex
DR HSSP;
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Best Local S
Matches 200
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Submitted (JUL-2002) to the EMBL/GenBank/DDBJ dat
EMBL; AX130282; AAN05026.1; -.
HSSP; Q9R435; 1HT2.
InterPro; IPR001466; Beta lactamase.
InterPro; IPR001871; Beta lactamase A.
Pfam; PF00144; Beta lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
PROSITE; PS001146; BETA LACTAMASE A; 1.
Q84H49 PRELIMINARY;
Q84H49;
01-JUN-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
TEM-110 beta-lactamase (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli
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255 AA;
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                                                                      PRELIMINARY;
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27906 MW;
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99.0%; Pred. No. 3.8e-77;
tive 1; Mismatches 1
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(TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation updataa-lactamase (Fragment).

update)

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Best Local
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BOX A.T.A., Paauw A., Leverstein-vanHall
Submitted (JUL-2002) to the EMBL/GenBank,
EMBL; AY130283; AAN05027.1; -.

HSSP; Q9R435; 1HTZ.
InterPro; IPR001466; Beta lactamase.
InterPro; IPR000871; Beta lactamase.
Pfam; PF00144; Beta-lactamase; 1.

PRINTS; PR00118; BLACTAMASEA.
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SEQUENCE
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SEQUENCE
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
TEM beta-lactamase (Fragment).
Acinetobacter sp. Ull.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                            Ghandili S., Hosseini-Mazinani S.M.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY583762; AAS86428.1; -.
HSSP; P00807; 1ALQ.
InterPro; IPR001466; Beta_lactamase.
InterPro; IPR000871; Beta_lactamase_A.
Pfam; PF00144; Beta-lactamase; 1.
                                                                                                                                                                                                                 PRINTS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE_A;
                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=U1
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moraxellaceae; Acinetobacter.
NCBI_TaxID=269266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q6PRU6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00146; BETA_LACTAMASE_A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192
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264 AA;
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261 AA;
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28986 MW;
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28738 MW;
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                                          Score 1027;
Pred. No. 4e-
1; Mismatches
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Pred. No. 3.9e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                A4F071CF7489352C CRC64;
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Mismatches 1
                                                Mismatches
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                                                                    7; DB 2;
4e-77;
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Best Local S
Matches 200
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A Yatsuyanagi J., Saito S., Harata S., Suzuki N., Amano K.-I.
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; AY538700; AAS46846.1; -.

REMBL; AY538701; AAS46847.1; -.

REMBL; AY538702; AAS46844.1; -.

REMBL; AY538698; AAS46848.1; -.

REMBL; AY538698; AAS46848.1; -.

REMBL; AY538698; AAS46848.1; -.

REMBL; AY538698; AAS46848.1; -.

REMBL; AY538701; AAS46848.1; -.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Serratia marcescens.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=blaTEM-1;
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QLIDWMEADKVAGPLLRSALPA
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Pred. No. 4.3e-77;
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Search completed: June 10, Job time : 68.6736 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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N	N	N	N	σ	7	7	7	N	N	ω	ω	N	N	S	σ	σ	N	N	4
AAY49892	AAW48613	AAY08232	AAY08234 ·	ABB82793	ADH14284	ADC22811	ADK65686	AAY06551	ADH11249	AAY70066	AAY70064	AAR52701	AAR88636	ADI46109	ADA67747	ABR55981	AAW18681	AAW16636	AAM84362
Aay49892	Aaw48613	Aay08232	Aay08234	Abb82793	Adh14284	Adc22811	Adk65686	Aay06551	Adh11249	Aay70066	Aay70064	Aar52701	Aar88636	Adi46109	Ada67747	Abr55981	Aaw18681	Aaw16636	Aam84362
RTEM with	Escherich	E. coli R	E. coli	Amino aci	Vector pc	Human G p		Escherich		Recombina	Recombina	. Plasmid p		Single st	Beta-lact	. hCG beta	. Membrane	Beta-lact	Human imm

ALIGNMENTS

AAE05544;

AAE05544 standard; protein;

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RESULT 1
AABOS544
ID AABO
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Cleavage-site
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(PANO-) PANORAMA RES

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CC (IdEA) systems that comparise a fusion sequence that encodes for a CC circularly permutated, interaction-activated proteins that reassemble to CC form functionally reconstituted marker proteins which produce a detectable signal upon the association of two oligopeptides, or upon CC simultaneous association of two oligopeptides with a third oligopeptide. CC The marker protein is preferably a type A beta-lactamase, especially TEM-CC 1 beta-lactamase of Escherichia coli. The oligopeptide is a member of a CC proteome library selected from single chain antibody Fortagment library, CC an antibody light chain variable region library and a peptide library and identifying interactions between intracellular as well as ccentrogropration of multiple genetic traits in a host cell. In particular, CC displayed within thioredoxin. The IdEA systems are useful for detecting crincorporation of multiple genetic traits in a host cell. In particular, CC displayes for the discovery and validation of pharmaceutics, collings. Frior systems (e.g. E. coli Dimer Detection System, yeast two-flowers for the discovery and validation of pharmaceutical targets and colings. Frior systems or Selective Infective phage System) require multiple steps between interaction and phenotype, which cause severe loss of efficiency class of efficiency due to high false positive and false negative rates. The present system or selective intracellular proteins in a high throughput system or metabolic or signal transduction pathways, in high crimical colings. The circularly permutated marker proteins in a high throughput steps between interaction of metabolic or signal transduction pathways, in high-throughput mapping of pair-wise protein-protein interactions within and in cell-based sensors for activation or signal transduction pathways, in high-throughput selection interaction. The present sequence is Escherichia coli consultation of interactions of any protein-protein interaction of activation of signal proteins of any cell-based server. Tem the beta-lactam
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                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-451857/48.
                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                     121
181
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                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                            KELTAFLHNMGDHYTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 180
                                                                                                                                                                                                                 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                                                                                                                                                                                                   HPETLVKVKDAEDQLGARVGYIBLDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                                                                                                                                                                                                                                                                                                                                                                                                                                      263 AA;
QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDG 228
                        QLIDWMEADKVAGPILRSALPAGWFIADKSGAGERGSRGIIAALGPDG 228
                                                                                                                                                                         AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                                                                                                                                                            HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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                                                                                                                                                                                                                                                                                                                                       100.0%; 5c.
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                    Score 1170; DB 4; Pred. No. 8.5e-117;
                                                                                                                                                                                                                                                                                                                                                  Mismatches
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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel fragment complementation system to identify interactions between polypeptides comprises fragment pairs having first and second members that reassemble into a marker protein which has a directly detectable that
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13-JAN-2000;
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DB; AAC90773.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
KELTAFIHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 180
                                                                                                                                                   AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                                                                                                                                                                                                    HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                                                                                                         AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                                                                                                                                                         HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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2000US-0175968P.
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                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1170; DB 4; 100.0%; Pred. No. 8.5e-117; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                 Índels
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KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ

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RESULT 3
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The invention describes a fragment complementation system (I) comprising CC a first oligopeptide having an N-terminal fragment with a C-terminal CC break-point, and a second oligopeptide having a C-terminal fragment with CC a N-terminal break-point, where the N-terminal fragment and the C-creminal fragment each are derived from a marker protein and reassemble CC to form a functionally reconstituted marker protein. (I) is useful for Selecting simultaneous incorporation of multiple genetic elements into a CC compound in a host. The method described is useful for identifying a Second oligopeptide to which a first oligopeptide binds, involving co-cexpressing the first and second oligopeptides. Binding of the first CC oligopeptide to the second oligopeptide results in the functional CC expression the occurrence of protein. The method is also useful for conitoring the occurrence of protein. The method is also useful for identifying oligopeptide interactions between two different proteomes; CC identifying oligopeptide interactions between two different proteomes; CC identifying epitopes that bind to an immunoglobulin variable region. (I) or an expression casette (II), encoding a selectable N or C-terminal peptide, is useful for identifying interactions between an extra cellular command of a transmembrane protein and a polypeptide, where the CC inhibit phosphorylation-regulated cell protein, preferably CD40. (I) or confidence in the cell protein in transducers. (I) or confidence in the cell protein of compound that confidence in the cell protein of compound that confidence in the cell protein of compound that cell inhibit phosphorylation-regulated cell signal transducers. (I)
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13-JAN-2000;
15-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fragment complementation system for detecting immunoglobulin epitope, has first oligopeptide containing N-terminal fragment with C-terminal break-point, second oligopeptide containing C-terminal fragment with N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fragment complementation system; marker protein; multiple genetic element incorporation; antibiotic resistance; beta-lactam derivative activation; anti-tumour compound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 2; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-SEP-2003; 2003US-00668778
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                                                                                                                                                                      Molecular chimaera for gene or virus directed enzyme prodrug therapy useful for treatment of cancer, viral infection or inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                          20-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
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                                                                                                                                                                                                                                                                                                                                                                              GROUP LTD
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Bscherichia coli beta-lactamase (AAW16634), including the signal peptide, is the expression product of a molecular chimaera, designated pCMV-BL (AAM766737), in which the beta-lactamase gene is under control of the CMV intermediate/early promoter. Vectors consisting of a transcriptional

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                           The intracellular form (AAW18680) of TEM beta-lactamase is expressed by pCMV-delBL (AAT70311) in which a PCR-amplified beta-lactamase coding sequence, minus the signal sequence, is placed under control of the intermediate/early promoter of cytomegalovirus. Intracellular beta-lactamase constructs, placed under control of promoter/enhancer elements
                                                                                                                                                                                                                                                                                                    DNA construct for gene-directed enzyme prodrug therapy of lung cancer comprises lung- or neuroendocrine-specific promoter controlling
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Pred. No. 8.5e-117;
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                                                                                                                                                                                                                                                                                                 In vitro method for testing mutagenicity of a chemical - by chemical cell line consisting of transformed fibroblasts had testable cytochrome P450 mixed function oxidase activity
                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                  Disclosure; Col 21-24; 24pp; English.
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04-JUN-1993
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circular; chimeric
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(first entry)
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1.5e-117;
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The expression constructs pRNH127 and pRNH155 contain identical sequences but were constructed using different strategies (see AAQ36498). The constructs comprise exons 2-7 of human CYP1A1 gene under the control of the inducible mouse metallothionein (MMT-1) promoter. The constructs also contain an open reading frame in the opposite orientation to the cytochrome P450 exons. This ORF encodes ampicillin resistance. The constructs are suitable for transformation of human fibroblasts derived from the xeroderma pigmentosum group A. Cultures of the transformed fibroblasts can be used to test substances for mutagenicity. The presence

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RARSULT 7
AAR9761
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XX Gene
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pCMV-BL (AAT29220), in which the beta-lactamase coding sequence is under the control of the intermediate/early cytomegalovirus promoter. Beta-lactamase delivery to mammalian cells confers sensitivity to cephalosporin prodrugs. Liposomal DNA/5-fluorouracil prodrug combinations resulted in s.c. tumour regression in mice bearing A549 tumours. Survival of mice bearing human large cell lung H460 intrathoracic (i.t.) tumours was increased upon i.t. injection of the secretory beta-lactamase DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the inducible cytochrome P450 gene allows metabolism of the substance to mutagenic metabolites. (Updated on 10-MAR-2003 to add missing OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene therapy; gene directed enzyme prodrug therapy; GDEPT; virus directed enzyme prodrug therapy; VDEPT; prodrug activation; cytotoxic; cytostatic; cancer; tumour; retrovirus; vector;
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                                                                                                                                                                                                                                                                                                                                       Molecular chimaera for use in enzyme gene therapy - is activated in target cell to express a secretable enzyme which cleaves a prodrug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Secretory beta-lactamase
                                                                                                                                                                                                A secretory beta-lactamase (AAR97619) is expressed from DNA construct
                                                                                                                                                                                                                                                     Example 3; Page 57-58; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (WELL )
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                                                                                                                                                                                                                                                                                                             the cell into a cytotoxic or cytostatic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                            AAT29220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WELLCOME FOUND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moore JT,
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Pred. No. 9.5e-117;
); Mismatches 0;
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RESULT 8
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.. Best Local Simi
Matches 228;
cytochrome P450IAI (CYPIAI) expression construct. Two clones, pRNH127 and pRNH15, were isolated by different methods and which both had the same sequence. The CYPIAI construct is used in assays to test for cytotoxicity of humans to a chemical. The method comprises exposing human fibroblast cells normally not including any cytochrome P450 activity to potentially toxic chemicals. The cells having been transformed to express cytochrome P450, under the control of a controllable promoter through the CYPIAI gene, upon exposure to the chemical in vitro. The chemical is metabolised intracellularly into a cytochrome metabolite by oxidation within the
                                                                                                                                                                                                                                                                                                                                                    Testing chemicals for cytotoxicity to human by using recombinant fibroblasts transformed with control of inducible promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 286
                                                                                                                                                                                                                                              The present sequence is encoded by a chimeric mouse metallothionein-
                                                                                                                                                                                                                                                                                                    Disclosure; Col 17-24; 26pp; English
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09-DEC-1992;
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25-NOV-1996
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DB; AAT30354.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novak RF,
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Pred. No. 9.5e-117;
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                                  Escherichia coli beta-lactamase (AAW16635), lacking the signal peptide, is the expression product of a molecular chimaera, designated pCMV-delBL (AAT66738), in which the beta-lactamase gene is under control of the CMV intermediate/early promoter. Vectors consisting of a transcriptional regulatory DNA sequence linked to a beta-lactamase gene can be used for enzyme prodrug therapy. Intracellular expression of the beta-lactamase in a targetted cell allows conversion of a prodrug into an agent toxic to the cell for treatment of cancer, viral (e.g. HIV) infection or
                                                                                                                                                                                                                                                                                                                          Molecular chimaera for question treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                        Example;
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                  the cell for inflammation
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s directed enzyme prodrug therapy;
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Pred. No. 9.5e-117;
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'maera, designated
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                  The secreted form (AAW18679) of TEM beta-lactamase is expressed by BL (AAT70309) in which a PCR-amplified beta-lactamase coding sequenglaced under control of the intermediate-learly promoter of cytomegalovirus. Secretory beta-lactamase constructs, placed under control of promoter/enhancer elements of lung-associated protein control of promoter/enhancer elements of lung-associated protein.
                                                                                                                                                                                               DNA construct for gene-directed enzyme prodrug therapy of lung cancer comprises lung- or neuroendocrine-specific promoter controlling \cdot expression of prodrug-converting enzyme.
                                                                                                                                                                                                                                                                                               N-PSDB;
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Best Local
This invention describes a novel tetracycline assay that uses recombinant prokaryotic cells comprising a luciferase gene under the transcriptional control of a tetracycline repressor and tetracycline promoter and involves the detection of luminescence emitted form the cells. The assay can be used to distinguish tetracycline form other microbial agents. The invention also describes a novel plasmid comprising either the luxCDABE genes, a tetracycline repressor (TetR) and a tetracycline repressor (TetR) and a tetracycline promoter (TetR) and a tetracycline assay method can be used for the determination of tetracycline in a sample,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Firefly; luciferase; tetracycline; transcriptional control; TetA; TetA; tetracycline repressor; tetracycline promoter; luminescence; luxCDABE; insect; Tn10; medicine; dosage; cheese production; antibiotic; foodstuf.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e.g. to study the dosage and penetration of the mechanism because also be used to test cheese production, as cheese making bacteria are not able to work in the presence of tetracycline. The method can also be used to determine the presence or concentration of antibiotics in foodstuffs, e.g. for allergic people. The present assay method does not rely on the growth of microbes as do conventional tests, and so is much more rapid. The present assay is also more sensitive, as even a small amount of luminescence can be detected
                                                                                                                                                                                                      Selecting monoclonal antibodies, hybridomas attached to antibody-lantibody library.
                                                                                                                                                                                                                                                                                                                                                                                           Breitling F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DE19900635-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Expression vector; antibody
B lymphocyte; myeloma cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Expression vector
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB10442 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 286 AA;
                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JAN-1999;
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                                                                                                                                                                                                                                                                                                                     AAA71430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  KREBSFORSCHUNGSZENTRUM.
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                                                                                                                                                                                                                                                                                                                                                                                              Poustka
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                                                                                                                                                                                                                                   antibody-binding
                                                                                                                                                                                                                                                                                                                                                                                                 Moldenhauer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            binding protein; monoclonal antibody; Neo-R; hybridoma; protein G; bla protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286
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Pred. No. 9.5e-117;
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                                                                                                                                                                                                                                                            by expressing them on the surface
                                                                                                                                                                                                                                   protein, then reaction
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This invention describes a novel method for the selection of monoclonal antibodies (MAb) which comprises (i) fusing B lymphocytes with myeloma cells to produce antibody-producing hybridomas such that the antibodies are presented at the surface of the hybridomas by an antibody-binding protein (I); and (ii) binding the antibody to antigens (Ag). The

Claim 16;

Fig 3; 22pp; German.

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Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 286 AA;
                                                                                     Selecting monoclonal antibodies, hybridomas attached to antibody-l
                                                                                                                                            N-PSDB; AAA71428.
                                                                                                                                                              WPI; 2000-499832/45.
                                                                                                                                                                                                  Breitling F,
                                                                                                                                                                                                                                                                             11-JAN-1999;
                                                                                                                                                                                                                                                                                                                  11-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                        13-JUL-2000.
                                                                                                                                                                                                                                                                                                                                                                                              DE19900635-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expression vector; antibody binding protein; monoclonal antibody; Neo-R; B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB10438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB10438 standard; protein;
                                                                 antibody library.
                                                                                                                                                                                                                                         (DEKR-) DEUT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vector
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                                                                                                                                                                                                                                         KREBSFORSCHUNGSZENTRUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                  Poustka A,
                                                                                                                                                                                                                                                                                                                  99DE-01000635
                                                                                                                                                                                                                                                                             99DE-01000635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pSEX11L4 bla protein.
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                                                                                 ntibodies, by expressing them on the surface of antibody-binding protein, then reaction with
                                                                                                                                                                                                   Moldenhauer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1170; DB 3; Pred. No. 9.5e-117;
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Claim 16; Fig 1; 22pp;

German

Selecting monoclonal antibodies, by expressing them on the surface

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC This invention describes a novel method for the selection of monoclonal CC antibodies (MAb) which comprises (i) fusing B lymphocytes with myeloma CC cells to produce antibody-producing hybridomas such that the antibodies CC are presented at the surface of the hybridomas by an antibody-binding protein (I); and (ii) binding the antibody to antigens (Ag). The CC invention also describes antibody-binding proteins (I) that comprise a CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa CC chain or a murine MHC (major histocompatibility complex) Class I k(k) CC molecule; an antibody-binding site of proteins A, G, L or LG, and the CC continents of PDGFR (platelet-derived growth factor receptor) CC or CD52. The method is used to select MAb with specificity for particular CC continents be made against many antigens in a library, optionally on CC mixtures of hybridomas can be used for selection, reducing the time and CC mixtures of hybridomas can be used for selection, reducing the time and CC cost involved in MAb selection. This sequence represents the Neo-R CC protein contained in the expression vector pSEXILL4 which contains the CC bla protein, Neo-R and protein G described in the method of the invention
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Matches
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N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB10440 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 286
                                                                                                                                                     11-JAN-1999;
                                                                                                                                                                                     11-JAN-1999;
                                                                                                                                                                                                                        13-JUL-2000.
                                                                                                                                                                                                                                                          DE19900635-A1
                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                          Expression vector; antibody binding protein; monoclonal antibody; Neo-R; B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.
                                                                                                                                                                                                                                                                                                                                                                              Expression vector pSEX11G2 bla protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                           26-MAY-1999;
                                                                                                                              26-MAY-2000;
                                                                                                                                                                                   30-NOV-2000
                                                                                                                                                                                                                                 WO200071729-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein encoded by bla resistance marker of integration vector pLO12306.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB50898 standard; protein; 286 AA.
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                          (UYFL ) UNIV FLORIDA RES FOUND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polymucleotide encoding a polymacharase under the transcriptional control of a surrogate promoter capable of increasing expression of the polysaccharase. The host cell also contains a second heterologous polymucleotide encoding a secretory polypeptide to facilitate the secretion of the expressed polysaccharase. The recombinant host cell is useful for producing polysaccharase which is useful for enzymatically degrading oligosaccharides such as lignocellulose, hemicellulose, cellulose, pectin or their combinations, and fermenting the product to ethanol, by simultaneous saccharification and fermentation processes. The present sequence is encoded by an integration vector which was introduced into cells to generate recombinant host cells. The vector contains a surrogate promoter from Zymomonas mobilis, the celZ gene from Erwinia chrysanthemi, resistance markers bla and tet, and Klebsiella oxytoca
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 286 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 82-83; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polysaccharase under control of surrogate promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant host cells useful for producing polysaccharase for degrading oligosaccharides, comprises a first heterologous polynucleotide encoding
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294 2 S1553 288 2 JQ1136 304 2 A49789 304 2 A35001 304 2 A35001 304 2 S06967 288 2 JS0755 305 2 A61556 305 2 A57002 305 2 A57002 305 2 JH0250 276 2 JH0258 291 2 JP0074 263 2 S23929 294 2 S19006 307 1 PNBSL	445.5	448.5	449.5	452.5	455	456.5	462	462	462	463.5	467.5	467.5	470.5	470.5	474.5	475.5
2 S16553 2 JQ1136 2 A49789 2 A49789 2 A35001 1 B45822 2 S06967 2 JS0755 2 A61156 2 A57002 2 A60680 2 JH0268	38.1	38.3	38.4	38.7	38.9	39.0	39.5	39.5	39.5	39.6	40.0	40.0	40.2	40.2	40.6	40.6
316553 JQ1136 A49789 A49789 A35001 B45802 S06967 JS0755 A61156 A57002 A60680 JH0268 JP0074 S2929 S19906 SNBSL	307	294	263	291	276	311	305	305	305	288	314	306	304	304	288	294
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beta-lactamase	PNBSL	S19006	S23929	JP0074	JH0268	JN0520	A60680	A57002	A61156	JS0755	S06967	B45822	A35001	A49789	JQ1136	816553

ALIGNMENTS

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beta-lactamase (EC 3.5.2.6) - phage phi-X174
C;Species: phage phi-X174
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S47061
R;Henrich, B.; Schmidtberger, B.
submitted to the EMBL Data Library, July 1994
A;Description: A variant of phiX174 gene E-based positive selection vectors with enhanced A;Reference number: S47060
A;Accession: S47061
                                                                                                                                                                        RESULT 2
S47061
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A;Title: Heterologous HIS3 marker and GFP reporter modules for PCR-target; A;Reference number: Z09587
A;Accession: T51301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: bla
C;Superfamily: beta-lactamase
C;Keywords: hydrolase
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C;Genetics:
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A; Residues: 1-286 <WAC>
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                                                                                                                                                                                                                                                      QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDG
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C;Species: Syntherry
C;Date: 25-Dec-1994 #Bequence_revision Zz-Auy-_____
C;Date: 25-Dec-1994 #Bequence_revision Zz-Auy-_____
C;Accession: S41975
R;Kacestner, K.H.; Montoliu, L.; Kern, H.; Thulke, M.; Schutz, G.
Gene 148, 67-70, 1994
A;Title: Universal beta-galactosidase cloning vectors for promoter
A;Title: Universal beta-galactosidase cloning vectors for promoter
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A;Molecule type: DNA
A;Residues: 1-286 <HEN>
A;Cross-references: UNIPROT:Q38058; EMBL:Z35638; NID:g520996; PIDN:CAA84692.1; PID:g5209
C;Superfamily: beta-lactamase I
C;Keywords: hydrolase
N;Alternate names: beta-lac
C;Species: Escherichia coli
C;Date: 30-Nov-1980 #sequen
                                                    beta-lactamase (EC 3.5.2.6) precursor - N;Alternate names: beta-lactamase TEM-6
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A;Residues: 1-266 <KAE>
A;Cross-references: EMBL:X76682; NID:9453622; PIDN:CAA54104.1; PID:9453623
A;Note: submitted to the EMBL Data Library, December 1993
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Matches
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;Date: 25-Dec-1994 #sequence_revision 22-Aug-1996 #text_change 20-Oct-2000
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                                                                                                                                                                                        QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDG 228
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ilarity 100.0%;
Conservative C
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                 #text_change 16-Aug-2004
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A;Molecule type: DNA
A;Rosidues: 1-101,'K',103-161,'H',163-286 <GOU>
A;Cross-references: EMBL:X57972; NID:g41816; PIDN:CAA41038.1; PID:g41817
A;Experimental source: ISI-like blaT-6 DNA
R;Sutcliffe, J.G.
Cold Spring Harb. Symp. Quant. Biol. 43, 77-90, 1979
A;Title: Complete nucleotide sequence of the Escherichia coli plasmid pBI
A;Reference number: A90923; MUID:80002802; PMID:383387
A;Contents: annotation
C;Comment: Like most penicillinases from gram-negative bacteria, this en:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Goussard, S.; Sougakoff, W.; Mabilat, C.; Bauernfeind, A.; Courvalin, P.
J. Gen. Microbiol. 137, 2681-2687, 1991
A;Title: An IS1-like element is responsible for high-level synthesis of extended-spectrum A;Reference number: S24415; MUID:92166702; PMID:1665171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Bacteriol. 172, 3040-3050, 1990

A;Title: The kil-kor regulon of broad-host-range plasmid RK2: nucleotide sequence, A;Reference number: A35387; MUID:90264294; PMID:2160936

A;Accession: A35387
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R;Sutcliffe, J.G.
R;Sutcliffe, J.G.
Proc. Natl. Acad. Sci. U.S.A. 75, 3737-3741, 1978
A;Title: Nucleotide sequence of the ampicillin resistance gene of Escherichia coli plasmi
A;Reference number: A93821; MUID:79012484; PMID:358200
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C; Keywords: antibiotic resistance; hydrolase; membrane protein
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A;Residues: 24-36,'K',38-286 <AMB>
A;Esperimental source: plasmid R6K
R;Kornacki, J.A.; Burlage, R.S.; Fi
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A;Status: translation not shown
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R;Goussard, S.; Sougakoff, W.; Mabilat, C.; Bauernfeind, A.;
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A;Residues: 182-286 <KOR>
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                            QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDG
                                                                                                     KELTAFLHIMGDHVTRLDRWEPELNEAI PNDERDTTMPAAMATTLRKLLTGELLTLASRQ
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Pred. No. 2.2e-93;
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C;Accession: S60312
R;Chanal, C.; Poupart, M.C.; Sirot, D.; Labia, R.; Sirot, J.; Cluzel, R.
Antimicrob. Agents Chemother. 36, 1817-1820, 1992
A;Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.
A;Reference number: S60310; MUID:93037315; PMID:1416873
A;Accession: S60312
A;Status: preliminary; translation not shown
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A;Residues: 1-286 <RES>
A;Cross-references: EMBL:U21228; NID:g885956; PIDN:AAA70411.1; PID:g885958
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Plasmid 29, 241-244, 1993
A;Title: Development of a native plasmid as a cloning vector A;Reference number: I40904; MUID:93361581; PMID:7689234
A;Accession: I40905
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A;Note: cloning vector pCG1408 engineered and expressed in Clavibacter xyli subsp.
C;Date: 15-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Oct-2000
C;Accession: I40905
C;Accession: I40905
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A; Residues: 1-286 < CHA>
A; Cross-references: EMBI
C; Superfamily: beta-lact
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  QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDG 228
                                                                KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLIGELLTLASRQ 180
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Pred. No. 2.2e-93;
1; Mismatches 1;
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Pred. No. 2.9e-92;
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R;Mabilat, C.; Lourencao-Vital, J.; Goussard, S.; Courvalin, P. Mol. Gen. Genet. 235, 113-121, 1992
A;Title: A new example of physical linkage between Tn1 and Tn21: A;Reference number: S30112; MUID:93062798; PMID:1331747
A;Accession: S30113
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                                                                                                                                                                                                                                                                                                                          C;Accession: S60310

R;Chanal, C.; Poupart, M.C.; Sirot, D.; Labia, R.; Sirot, A; Poupart Antimicrob. Agents Chemother. 36, 1817-1820, 1992

A;Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7

A;Reference number: S60310; MUID:93037315; PMID:1416873
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C;Superfamily: beta-lactamase I
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A; Residues: 1-286 < MJ
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Similarity 97.8%;
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AGQEQLGRRIHYSQUDLVEYSPVTEKHLTDGMTVRELCSAAIIMSDUTAAULLLTTIGGP
                                                              HPETLVKVKDAEDKLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRVD
                                                                                    HPETLYKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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                                                                                                                                                      97.9%;
                                                                                                                                    ; Score 1145; D
; Pred. No. 1.2e
3; Mismatches
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Pred. No. 3.5e-92;
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.2e-91;
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Protein - Salmonella typhimurium plasmid NTF N; Alternate names: beta lactamase homolog C; Species: Salmonella typhimurium C; Date: 30-Sep-193 #sequence_revision 30-Sep-199 C; Accession: JQ1546 R; Cannon, P. M.; Strike, P. Plasmid 27, 220-230, 1992 A; Title: Complete mucleotide sequence and gene org. A; Reference number: JQ1538; MUID:92383313; PMID:13: A; Accession: JQ1546 A; Status: translation nor ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          beta-lactamase
C;Species: Klebs
C;Date: 12-Apr-1
C;Accession: S60
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A;Residues: 1-32 <TOL>
A;Cross-references: GB:M55547; NID:g155010; PIDN:AAA98408.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 12-Apr-1996 #sequence revision 19-Apr-1996 #text_change 09-Jul-2004 C;Accession: $60311; F37392; PQ0498 R;Chanal, C.; Poupart, M.C.; Sirot, D.; Labia, R.; Sirot, J.; Cluzel, R. Antimicrob. Agents Chemother. 36, 1817-1820, 1992 A;Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase gen. A;Reference number: $60310; MUID:93037315; PMID:1416873 A;Accession: $60311
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Plasmid 24, 218-226, 1990
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Best Local Similarity
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;Species: Klebsiella pneumoniae
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                                                                                                                                                                                                                                                                             QLIDWMEADKVAGPLLRSALPAGWFIADKSGTGKRGSRGIIAALGPDG
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milarity 96.9%;
Conservative
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Pred. No. 1.7e-91;
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                                                      gene organization
; PMID:1325061
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                   beta-lactamase (EC 3.:
N;Alternate names: bet
C;Species: Klebsiella
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S16146
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C; Genetics:
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A; Residues: 1-265
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C; Superfamily:
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A;Residues: 1-286 <CAN>
A;Cross-references: UNIPROT:Q8L2F9
C;Genetics:
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A;Genome: plasmid
C;Superfamily: beta-lactamase I
C;Keywords: antibiotic resistance; hydrolase
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Biochem. J. 251, 73-79, 1988
A;Tille: Complete amino acid sequence of p453-plasmid-mediated
A;Reference number: S00464; MUID:88268817; PMID:3260490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1993
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                                                                                                                         ELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQQ 181
                                                                                                                                                                                                                               GQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGFK 121
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LIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPD
                                                              GLTAFLRQIGDNVTRLDRWETELNEALÞGDARDTTTÞASMAATLRKLLTSQRLSARSQRQ
                                                                                                                                                                                       GDEQLERKIHYRQQDLVDYSPVSEKHLADGMTVGELCAAAITMSDNSAANLLLTAVGGPA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                          70.8%; Score 828; DB 2; 69.0%; Pred. No. 3.1e-64; tive 33; Mismatches 37
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Pred. No. 3.9e-91;
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-VHS

Klebsiella

pneumoniae

plasmids

82 61

202 181

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RiGarbarg-Chenon, A.; Godard, V.; Labia, R.; Nicolas, J.C. Antimicrob. Agents Chemother. 34, 1444-1446, 1990
A;Title: Nucleotide sequence of SHV-2 beta-lactamase gene. A;Reference number: A60679; MUID:90351141; PMID:2201259
A;Accession: A60679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-30,'L',32-286 <LBE>
A;Cross-references: GB:X62115; NII:g48988; PIDN:CAA44025.1; PID:g48990
A;Experimental source: plasmid BWH77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Cross-references: EMBL:X53817; NID:g43795; PIDN:CAA37813.1; PID:g43796
A;Experimental source: plasmid pZMP1
R;Lee, K.Y.; Hopkins, J.D.; Syvanen, M.
J. Bacteriol. 172, 3229-3236, 1990
A;Title: Direct involvement of IS26 in an antibiotic resistance operon.
A;Reference number: A35395; MUID:90264317; PMID:2160941
A;Accession: A35395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 15-Oct-1999 (;Accession: S16146; A35395; S18767 R;Podbielski, A.; Schoenling, J.; Melzer, B.; Warnatz, K.; Leusch, H.G. J. Gen. Microbiol. 137, 569-578, 1991 A;Title: Molecular characterization of a new plasmid-encoded SHV-type beta-1A;Reference number: S16146; MUID:91237320; PMID:2033379 A;Accession: S16146
                                                                                                                                                                                                                                                                                                                                                                                                                            beta-lactamase (EC 3.5.2.6) SHV-2 precursor - Salmonella typhimurium plasmid C;Species: Salmonella typhimurium C;Decies: Salmonella typhimurium C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Aug-2004 C;Accession: A60679
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                                                                                                                                  ;Genome: plasmid
;Superfamily: Beta-lactamase I
;Keywords: antibiotic resistance; hydrolase
                                                                                                             ;1-21/Domain: signal sequence #status
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;Superfamily: beta-lactamase I
;Keywords: antibiotic resistance; hydrolase
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                                            Query Match
Best Local 9
                     70.6%; Score 826; DI
Local Similarity 68.6%; Pred. No. 5.1e
198 155; Conservative 33; Mismatches
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Similarity 68.6%; Pred. No. 5.1e-64;
55; Conservative 33; Mismatches 38
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                                          5.1e-64;
                                                                 DB 2; Length 286;
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A44998
A;Residues: 1-286 <hUL>
A;Residues: 1-286 <hUL>
A;Residues: 1-286 <hUL>
A;Croos-references: UNIPROT:P14558; GB:M95179; NID:g150488; PIDN:AAA25526.1; PID:g150489
A;Croos-references: UNIPROT:P14558; GB:M95179; NID:g150488; PIDN:AAA25526.1; PID:g150489
A;Podbielski, A.; Melzer, B.
Nucleic Acids Res. 18, 4916, 1990
A;Title: Nucleotide sequence of the gene encoding the SHV-2 beta-lactamase (bla(SHV-2)) of A;Reference number: S12703; MUID:90370479; PMID:2395654
                                                                                                                                                                            R;Huletsky, A.; Couture, F.; Levesque, R.C. Antimicrob. Agents Chemother. 34, 1725-1732, 1990
A;Title: Nucleotide sequence and phylogeny of SHV-2 beta-lactamase A;Reference number: A44998; MUID:91136192; PMID:2285285
A;Accession: A44998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEBS Lett. 231, 217-220, 1988
A;Title: Single amino acid substitution between SHV-1 beta-lactamase
A;Reference number: S02434; MUID:88196385; PMID:3129309
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C;Accession: A44998; S12703
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C;Species: Bscherichia coli
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993
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A;Genome: plasmid
C;Superfamily: Beta-lactamase I
C;Keywords: antibiotic resistance; hydrolase
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A;Status: translation not shown
A;Status: translation not shown
A;Rolecule type: DNA
A;Residues: 1-286 <POD>
A;Cross-references: EMBL:X53433; NID:g43789; PIDN:CAA37524.1; PID:g43790
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       92
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   RESULT 2
Q6WWY4
ID Q6WW
AC Q6WW
DT 05-J
DT 05-J
O6WWY4 PRELIMINARY; PRT; 232 AA.
Q6WWY4;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
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	Query I Best Lo Matche	SEQUEN STRAIN Obert Submit Submit EMBL; HSSP; Interp PRINTS PROSIT NON TE NON TE SEQUEN	05 05 05 Nam Klel Bact Rhtel NCB	RESULT 1 Q6WWY5 ID Q6W	00000000004444 00000000400000000000000
61 AG 	y Match Local Sim nes 228; 1 HP:	சல் இரு குடி	05-JUL-2004 (Tr 05-JUL-2004 (Tr 05-JUL-2004 (Tr 05-JUL-2004 (Tr Beta-lactamase NameeblaTEM; Klebsiella oxyt Bacteria; Prote Enterobacteriac NCBI_TaxID=571;	ል የ የ የ የ የ የ የ የ የ የ የ የ የ የ የ የ የ የ የ	1165 1165 1165 1165 1165 1165 1162 1162
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HYSQNE HYSQNE GDHVTH GDHVTH GDHVTH WAGPLL	100. 100. ative ABDQLG 	ne C) to 9384 ; Be ACTA ETA_ 229 250	TEMBLrel. 27, Cre TEMBLrel. 27, Las TEMBLrel. 27, Las (Fragment). (Fragment). toca. eobacteria; Gamma ceae; Klebsiella	NARY;	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
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AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLITTIGGP 120	100.0%; Score 1170; DB 2; Length 229; illarity 100.0%; Pred. No. 8.7e-87; Conservative 0; Mismatches 0; Indels 0; Gaps 0 ETILVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60	databases.	date) date) Bnterobacteriales;		Q7bp57 shigella fl Q7br75 neisseria m Q7dfy3 salmonella Q7dhd3 serratia ma Q7ghd3 serratia ma Q7991 plasmid pet Q6wwy6 citrobacter P7814 escherichia Q8ksd2 escherichia Q8ksd2 escherichia Q6q4t6 pseudomonas Q9khc0 escherichia Q32372 capnocytoph Q8rpy9 enterobacte Q932y6 pseudomonas

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                                                                                                                              PRINTS; PRO0118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE_A;
                                                                                                                                                                              InterPro; IPR001466; Beta lactamase. InterPro; IPR000871; Beta lactamase A. Pfam; PF00144; Beta-lactamase; 1.
                                                                                                                                                                                                                                                EMBL; AY265882; AAP93840.1;
HSSP; P00807; 1KGE.
                                                                                                                                                                                                                                                                                           STRAIN=MISC112;
Obert C.A., Goldstone C.M.,
Submitted (APR-2004) to the
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Klebsiella pneumoniae.
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PRINTS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA LACTAMASE A; 1.
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O6WWY3; PREVININARY; PRT; 242 AA.
O5-JUL-2004 (TrEMBLrel. 27, Created)
O5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
O5-JUL-2004 (TrEMBLrel. 27, Last annotation updat
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Obert C.A., Goldstone C.M.,
Submitted (APR-2004) to the
EMBL; AY265887; AAP93845.1;
HSSP; P00807; 1KGE.
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NON_TER 1 1 1
NON_TER 242 242
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Name=blaTEM;
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242 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1170; DB 2;
Pred. No. 9.3e-87;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein (Fragment).
Hypothetical protein (Fragment).
Hordeum vulgare (Barley).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae, Streptophyta; Poales, Pooidea,
                                        HSSP; Q9R435; 1HTZ.
InterPro; IPR001466; Beta_lactamase. InterPro; IPR000871; Beta_lactamase_A.
Pfam; PF00114; Beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
                                                                                                                                                                                                                                                                               MEDIINE=95172401; PubMed=7867948; DOI=10.1016/0378-1119(94)00839-K; Henrich B., Schmidtberger B.;
"A variant of phiX174 gene B-based positive selection vectors with enhanced lytic potential.";
Gene 154:51-54(1995).
Gene 154:51-54(1995).
EMBL; Z35638; CAA84692.1; -.
EMBL; Z35638; CAA84692.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriophage phi-X174.
Viruses; ssDNA viruses; Microviridae;
NCBI_TaxID=10847;
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01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
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Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ717739; CAG30723.1; -.
HSSP; P00807; 1ALQ.
InterPro; IPR001466; Beta lactamase.
InterPro; IPR001466; Beta lactamase.
Pfam; PF00144; Beta-lactamase; 1.
PFINTS; PR00114; Beta-lactamase; 1.
PRINTS; PR00118; BETA-LACTAMASE,
PROSITE; PS00146; BETA-LACTAMASE,
PROSITER; PS00146; BETA
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Name=bla;
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BETA_LACTAMASE_A; 1
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Pred. No. 1.1e-86;
); Mismatches 0;
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Best Local S
Matches 228
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Best Local :
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PLASMID=J3356/pOX7/3, and J3356/POX7/1;
PLASMID=J3356/pOX7/3, and J3356/POX7/1;
MEDLINE=96422755; PubMed=8825372; DOI=10.1006/plas.1995.0005;
MEDLINE=96422755; PubMed=8825372; DOI=10.1006/plas.1995.0005;
Needham C., Noble W.C., Dyke K.G.;
"The staphylococcal insertion sequence IS257 is active.";
"The staphylococcal insertion sequence IS257 is active.";
Plasmid 34:198-205(1995);
EMBL; U36912; AAB39956.1; -.
EMBL; U36911; AAB39956.1; -.
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Q00626; O08022; O08102; O09393; O09396; O09397; O09398;
O09400; O09401; O09402; O09403; O09404; O09406;
O09408; O09481; O09482; O09483; O09490; O57339;
O1-NOV-1996 (TYEMBLTel. 01, Last sequence update)
25-OCT-2004 (TYEMBLTel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001466; Beta lactamase. InterPro; IPR000871; Beta lactamase. A. Pfam; PF00144; Beta-lactamase; 1.
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                                                                                             KELTAFLHNMGDHVTKLDRWEPELNEAI PNDERDTTMPVAMATTLRKLLTGELLTLASRQ
                                                                                                                       KELTAFLHNMGDHVTRLDRWBPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ
                                                                                                                                                                                           AGOEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
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Bacillales; Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                           Score 1170; DB 2;
Pred. No. 1.1e-86;
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Pred. No. 1.1e-86;
; Mismatches 0;
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RESULT
Q79DR3
ID Q7
AC Q7
AC Q7
DT 05
DT 05
DT 95
DT 85
C DF M6
GN N6
GN
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Q79CL6
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Best Local Similarity
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079CL6;
05-JUL-2004
05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                         Q79DR3
Q79DR3;
                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Mutant extended-spectrum beta-lactamase precursor (
Name=bla; Synonyms=blaTEM-116;
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serebrijski I., Vassin V., T
Submitted (JUL-1995) to the
EMBL; U31280; AAC44581.1; -.
HSSP; P00807; 1ALQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97074643; PubMed=8917070; DOI=10.1016/0378-1119(96)00114-X; Serebrijski I.G., Vassin V.M., Tsygankov Y.D.; "Two new members of the BioB superfamily: cloning, sequencing and expression of bioB genes of Methylobacillus flagellatum and Corynebacterium glutamicum."; Gene 175:15-22(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001466; Beta_lactamase.
InterPro; IPR000871; Beta_lactamase_A.
Pfam; PF00144; Beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE A; 1.
SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;
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Bacteria; Proteobacteria; Betaproteobacteria; Methylophilales;
Methylophilaceae; Methylobacillus.
                          SEQUENCE
                                                                                                                         Plasmid pRP4, and Plasmid pCAPs.
Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beta-lactamase.
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                                                                        NCBI_TaxID=562;
                                                                                                      Enterobacteriaceae;
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                                                                                                      Escherichia
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27,
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Last sequence update)
Last annotation update)
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Pred. No. 1.1e-86;
); Mismatches 0;
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RESULT
Q84H50
ID Q8
AC Q8
DT 01
DT 01
DT 01
DT 11

10

Q84H50; Q84H50; 01-JUN-2003 01-JUN-2003 01-OCT-2003

PRELIMINARY;

PRT;

255

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TEM-117

beta-lactamase

(Fragment)

(TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)

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Best Local
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"Molecular Characterization of Extended-Spectrum Beta-Lactamases produced by Clinical Isolates of Klebsiella pneumoniae and Eschen coli from a Korean Nationwide Survey.";

J. Clin. Microbiol. 42:2902-2906(2004).

EMBL; W14750; AAA24057.1; -.

EMBL; W14750; AAA24057.1; -.

EMBL; AV42598; AAA25605.1; -.

EMBL; AV42598; AAA25605.1; -.

EMBL; AV42598; AAA25605.1; -.

EMBL; AV42598; AAA25605.1; -.
                                                                                                                                                                                                                                                                                                               GG; GO:0008800; Fibeta-lactamase activity; IEA.
GG; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR001466; Beta-lactamase.
InterPro; IPR00871; Beta-lactamase_A.
Pfam; PF00144; Beta-lactamase; 1.
PRINTS; PR00118; BIACTAMASEA.
PRINTS; P8001146; BETA-LACTAMASE_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98189310;
Schlieper D., Von
Mueller-Hill B.;
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Rondot S., Anthony K., Dubel S., Ida N., Beyro
Little M., Breitling F.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maneewannakul K., Maneewannakul S., Ippen-Ihler K.;
Submitted (AUG-1991) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                     Hydrolase; Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=15243036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anal. Biochem. 257:203-209(1998).
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Escherichia coli."
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                                                   KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTIMPVAMATTLRKLLTGELLTLASRQ 180
                     QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDG
                                                                                                           AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                                   AGQEQLGRRIHYSQNDLVEYSPVTEXHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDG
                                                                                                                                                                                                                                                                             286 AA;
                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             310; PubMed=9514792; DOI=10.1006/abio.1997.2558; Von Wilcken-Bergmann B., Schmidt M., Sobek H.,
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                                                                                                                                                                                                                                                                             31557 MW;
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                                                                                                                                                                                                                                                                                                     Signal.
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                                                                                                                                                                                                                                   Score 1170;
Pred. No. 1.
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                                                                                                                                                                                                                                   70; DB 2;
1.1e-86;
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 251
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Q8444
Q8444
AC Q8444
AC Q8444
DT 01-JU
DT 01-JU
DT 01-OC
DE TEM-1
OS Klebs
OC Bacte
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RP SEQUE
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Matches 226
                                          Query Match
Best Local Similarity
Matches 226; Conser
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Q84H49;
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NON TER
SEQUENCE
                                                                                                                                                 SEQUENCE FROM N.A.

BOOX A.T.A., Paauw A., Leverstein-vanHall M.A.,
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ d
EMBL; AY130283; AANOS027.1; -.

HSSP; Q9R435; 1HTZ;
InterPro; IPR0001466; Beta lactamase.
InterPro; IPR000187; Beta-lactamase_A.
Pfam; pF00144; Beta-Lactamase; 1.

PRINTS; PR00118; BLACTAMASEA.
                                                                                                                                                                                                                                                                                                                            01-JUN-2003 (TREMBLrel. 24, Create 01-JUN-2003 (TREMBLrel. 24, Last s. 01-OCT-2003 (TREMBLrel. 25, Last a. TEM-110 beta-lactamase (Fragment) Klebsiella oxytoca.
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Submitted (JUL-2002) to the EMBL/GenBank/DDBJ
EMBL; AY130282; AAN05026.1; -.
HSSP; Q9R435; 1HTZ.
                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Klebsiella.
                                                                                                                                  PROSITE; PS00146; BETA_LACTAMASE_A; 1.
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InterPro; IPR000871; Beta lactamase A.
Pfam; PF00144; Beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
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Enterobacteriaceae; Escherichia.
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llarity 99.1%;
Conservative
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llarity 99.1%;
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                                                                                              28738 MW;
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                                         ; Score 1165; DI
; Pred. No. 2.6e
1; Mismatches
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Pred. No. 2.5e-86;
1; Mismatches 1;
                                                                                              4F748F7733A08CBB
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RESULT 13
Q6QIVO
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DT 05-JU
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GN Name=
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Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
R EMBL; AY583762; AAS86428.1; -
R HSSP; P00807; 1ALQ.
InterPro; IPR001466; Beta lactamase.
R InterPro; IPR001871; Beta lactamase A.
R Pfam; PF00144; Beta-lactamase; 1.
R PRINTS; PR00118; BLACTAMASEA.
R PROSITE; PS00146; BETA LACTAMASEA; 1.
R NON TER 264 264
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Best Local (
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Q6QIVO PRELIMINARY; PRT; 281 AA. Q6QIVO; CFUL-2004 (TrEMBLrel. 27, Created) 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) TEM-1 beta-lactamase (Fragment).
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Bacteria; Proteobacteria; Gammaproteobacteria;
Moraxellaceae; Acinetobacter.
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Pred. No. 2.6e-86;
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Best Local Similarity
Matches 226; Conser
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Best Local
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G6QIV1;
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
                                                           PROSITE; PS00146; BETA LACTAMASE A; 1.
NON TER 281 281
SEQUENCE 281 AA; 30837 MW; C8934B9
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Submitted (FEB-2004) to the
EMBL; AY538699; AA846845.1;
HSSP; P00807; 1ALQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                Serratia marcescens.
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STRAIN=ES-42, ES-46,
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Enterobacteriaceae; Serra
                                                                                                                              InterPro; IPR001466; Beta lactamase.
InterPro; IPR000871; Beta lactamase A.
Pfam; PF00144; Beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
                                                                                                                                                                                                                                                                                                    STRAIN=ES-31;
                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=615;
                                                                                                                                                                                                                                                                                                                                                                                        Enterobacteriaceae; Serratia.
                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=blaTEM-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TEM-1 beta-lactamase
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InterPro; IPR000871; Beta_lactamase_A.
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S; PR00118; BLACTAMASEA.
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nilarity 99.1%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Serratia.
  99.6%;
99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Fragment).
                                                                                                                                                                                                                                                          Harata S., Suzuki N., Amano K.-I.;
he EMBL/GenBank/DDBJ databases.
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Pred. No. 2.8e-86;
1; Mismatches 1
  Score
Pred.
                                                                9B18934B9C696057
  1165;
No. 2
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  5; DB 2;
2.8e-86;
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21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
25-UAN-2005 (Rel. 46, Last annotation update)
Beta-lactamase TEM precursor (EC 3.5.2.6) (TEM-1) (TEM-2)
(TEM-4) (TEM-5) (TEM-6) (TEM-8/CAZ-2) (TEM-16/CAZ-7) (TEM-
SEQUENCE OF 24-286 (TEM-2);
PLASMID=R6K; TRANSPOSON=Th1;
MEDLINE=79012483; PubMed=358199;
Ambler R.P., Scott G.K.;
"Partial amino acid sequence of property of the sequence of
                                                                                                                                                MEDLINE-86319522; PubMed=3019092; DOI=10.1016/0065-227X(86)90018-3; Ohtsubo H., Ryder T.B., Maeda Y., Armstrong K., Ohtsubo E.; "DNA replication of the resistance plasmid R100 and its control."; Adv. Biophys. 21:115-133(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (TEM-1).
PLASMID=R1 (R7268); TRANSPOSON=Tn3;
MEDLINE=79012484; PubMed=358200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli.
Plasmid R1 (R7268), Plasmid InCFII R100, Plasmid R6K, Plasmid pUD16, Plasmid pCFF04, and Plasmid pCFF14.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                       PLASMID=IncFII
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=80002802;
Sutcliffe J.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (TEM-1).
PLASMID=R1 (R7268); TRANSPOSON=Tn3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Nucleotide sequence of the ampicillin resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sutcliffe J.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=562;
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                                                                                                                                                                                                                                                                                                                                                                             'Complete nucleotide sequence
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                            Spring Harb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plasmid pBR322.";
. Natl. Acad. Sci. U.S.A.
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  penicillinase
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MEDLINE=93361453; PubMed=8356032;
Jelsch C., Mourey L., Masson J.-M
"Crystal structure of Escherichia
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SEQUENCE FROM N.A. (TEM-4 AND TEM-5).
STRAIN=CB86134; PLASMID=PCFF04, and pUD16;
MEDLINE=89378760; PubMed=2550326; DOI=10.1016/0378-1119(89)90236-9;
MEDLINE=89378760; FubMed=2550326; DOI=10.1016/0378-1119(89)90236-9;
Sougakoff W., Petit A., Goussard S., Sirot D., Bure A., Courvalin P.;
"Characterization of the plasmid genes blaT-4 and blaT-5 which encode the broad-spectrum beta-lactamases TEM-4 and TEM-5 in
                                                  MEDLINE=96186252; PubMed=8605632;
Strynadka N.C.J., Jensen S.E., Alzari P.M., James M.N.G.;
"A potent new mode of beta-lactamase inhibition revealed by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93037315; PubMed=1416873; Chanal C., Poupart M.C., Sirot D., Labia R., Sirot J., Cluzel R.; "Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goussard S., Sougakoff W., Mabilat C., Bauernfeind A., Courvalin P.; "An IS1-like element is responsible for high-level synthesis of extended spectrum beta-lactamase TEM-6 in Enterobacteriaceae.";
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Mabilat C., Lourencao-Vital J., Goussard S., Courvalin P.;
Mabilat C. Lourencao-Vital J., Goussard S., Courvalin P.;
"A new example of physical linkage between Tn1 and Tn21: the
antibiotic multiple-resistance region of plasmid pCFF04 encoding
extended-spectrum beta-lactamase TEM-3.";
mol. Gen. Genet. 235:113-121(1992).
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X-ray crystallographic Nat. Struct. Biol. 3:29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF TEM-1.
MEDLINE=92183921; PubMed=1544485; DOI=10.1016/0014-5793(92)80232-6;
Velach C., Lenfant F., Masson J.-M., Samama J.-P.;
"Beta-lactamase TEM1 of E. coli. Crystal structure determination at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genes.";
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                                                                                                                                                                                                              Proteins
                                                                                                                                                                                                                                          resolution."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Characterization and amino acid sequence enzyme with a decreased susceptibility to FEMS Microbiol. Lett. 120:111-117(1994).
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                                                                                                                                                (-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      .5-A resolution."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasmid R6K.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78:339-348(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                       299:135-142(1992).
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J., Canica M.M.,
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hic structure of the 3:290-297(1996).
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                                                                                                                                                                                                                                                                    Masson J.-M., Samama J.-P.;
Escherichia coli TEM1 beta-lactamase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOI=10.1016/0378-1097(94)00186-3;
Paul G., Nevot P., Barthelemy M.,
                                                                                                                                                                                                                                                                                                                                                              OF TEM-1.
                                                                                                                                                   OF TEM-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to beta-lactamase inhibitors.";
                            TEM-1-BLIP
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                                                                                                                                                   COMPLEXED
                            complex.";
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EMBL; J01749; AAB59737.1;
EMBL; V00613; CAA23886.1;
EMBL; X64523; CAA45828.1;
EMBL; X57972; CAA41038.1;
EMBL; X65252; CAA46344.1;
EMBL; X65252; CAA46345.1;
EMBL; X65253; CAA46346.1;
EMBL; X65254; CAA46346.1;
EMBL; U89928; AAB64386.1;
EMBL; U66885; AAC48875.1;
                                                                                                                                                                                                                                                                                                     EMBL;
PIR;
PIR;
PDB;
PDB;
PDB;
"X-ray structure of the Asn276Asp variant of the Escherichia coli TEM-
1 beta-lactamase: direct observation of electrostatic modulation in
resistance to inactivation by clarvalanic acid.";
Biochemistry 38:9570-9576(1999).

-I- FUNCTION: TEM-type are the most prevalent beta-lactamases in
enterobacteria; they hydrolyze the beta-lactam bond in susceptible
beta-lactam antibiotics, thus conferring resistance to penicillins
and cephalosporins. TEM-3 and TEM-4 are capable of hydrolyzing
ceftazidime. TEM-6 scapable of hydrolyzing
ceftazidime and ceftazidime. TEM-5 scapable of hydrolyzing
ceftazidime. TEM-6 scapable of hydrolyzing
ceftazidime. TEM-6 scapable of hydrolyzing
ceftazidime and ceftazidime. TEM-5 scapable of hydrolyzing
ceftazidime and ceftazidime. TEM-5 scapable of hydrolyzing
ceftazidime and cefta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires
or send an email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restriuse by non-profit institutions as long as its content i modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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"Crystal structure of an acylation transition-state analog of the lbeta-lactamase. Mechanistic implications for class A beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS)
MEDLINE=98153145; PubMed=9485412; DOI=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BIOTECHNOLOGY: This protein is used as a marker in many used cloning vectors, such as pBR322 and the pUC series MISCELLANGOUS: The beta-lactamase present on pBR322 was from plasmid R1 (R7268)
                                                                                                                                                                                                                                                                                                                                      A93821;
S30113;
1AXB; X-
                                                                                                                 1BT5;
1BTL;
1CK3;
1ERM;
1ERO;
1ERO;
1ERO;
1ERO;
1FQG;
1FQG;
1JTG;
1JTG;
1JTG;
1JTG;
1JVJ;
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CATALYTIC ACTIVITY: A beta-lactam + H(2)0 = a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          active against ceftazidime. IRT-4 shows resistance to
                                                                 1JWZ;
1LHY;
1LIO;
               ; XXNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s requires a license agreement (S
an email to license@isb-sib.ch).
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S30113.
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